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<b>(21) International Application Number:</b> PCT/US92/08637 <b>(22) International Filing Date:</b> 15 October 1992 (15.10.92)  <b>(30) Priority data:</b> 07/777,859                      16 October 1991 (16.10.91)      US 07/881,396                      8 May 1992 (08.05.92)              US  <b>(71) Applicant:</b> IMMULOGIC PHARMACEUTICAL CORPORATION [US/US]; One Kendall Square, Building 600, Cambridge, MA 02139 (US).  <b>(72) Inventors:</b> Garman, Richard, D. ; 21 Fessenden Road, Arlington, MA 02174 (US). GREENSTEIN, Julia, L. ; 174 Mount Vernon Street, West Newton, MA 02165 (US). KUO, Mei-Chang ; 5 Cox Road, Winchester, MA 01890 (US). ROGERS, Bruce, L. ; 54 Richardson Road, Belmont, MA 02178 (US).		<b>(74) Agents:</b> CHANNING, Stacey, L. et al.; Immulogic Pharmaceutical Corporation, Patent Department, One Kendall Square, Building 600, Cambridge, MA 02139 (US).  <b>(81) Designated States:</b> AU, CA, FI, HU, JP, KR, NO, European patent (AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LU, MC, NL, SE).  <b>Published</b> <i>With international search report.</i>
<b>(54) Title:</b> T CELL EPITOPES OF THE MAJOR ALLERGENS FROM DERMATOPHAGOIDES (HOUSE DUST MITE)  <b>(57) Abstract</b>  The present invention provides isolated peptides of the major protein allergens of the genus <i>Dermatophagoides</i> . Peptides within the scope of the invention comprise at least one T cell epitope, or preferably at least two T cell epitopes of a protein allergen selected from the allergens <i>Der p</i> I, <i>Der p</i> II, <i>Der f</i> I, or <i>Der f</i> II. The invention also pertains to modified peptides having similar or enhanced therapeutic properties as the corresponding, naturally-occurring allergen or portion thereof, but having reduced side effects. The invention further provides nucleic acid sequences coding for peptides of the invention. Methods of treatment or of diagnosis of sensitivity to house dust mites in an individual and therapeutic compositions comprising one or more peptides of the invention are also provided.		

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## T CELL EPITOPES OF THE MAJOR ALLERGENS FROM DERMATOPHAGOIDES (HOUSE DUST MITE)

### Related Applications

This application is a continuation-in-part of U.S.S.N. 07/881,396 entitled "T Cell Epitopes of the Major Allergens From Dermatophagoides (House Dust Mite)", filed May 8, 1992, which is a continuation-in-part of U.S.S.N. 07/777,859 entitled "T Cell Epitopes of the Major Allergens From Dermatophagoides (House Dust Mite)", filed October 16, 1991, the teachings of which are incorporated herein by reference.

### Background of the Invention

Recent reports have documented the importance of responses to the Group I (e.g., Der p I and Der f I) and Group II (e.g., Der p II and Der f II) protein allergens in house dust mite allergy. For example, it has been documented that over 60% of patients have at least 50% of their anti-mite antibodies directed towards these proteins (e.g., Lind, P. et al., Allergy, 39:259-274 (1984); van der Zee, J.S. et al., Journal Allergy and Clinical Immunology, 81:884-896 (1988)). It is possible that children show a greater degree of reactivity to the Group I and Group II allergens (Thompson, P.J., et al., Immunology, 64:301-314 (1988)). Allergy to mites of the genus Dermatophagoides (D.) is associated with conditions such as asthma, rhinitis and ectopic dermatitis. Two species, D. pteronyssinus and D. farinae, predominate and, as a result, considerable effort has been expended in trying to identify the allergens produced by these two species.

A concerted effort has been made to characterize by gene cloning the major allergens from both D. pteronyssinus and D. farinae. Consequently, several publications have reported the complete nucleotide sequences of several allergens including Der p I (Thomas, W.R., et al., International Archives of Allergy and Applied Immunology, 85:127-129 (1988); and Chua, K.Y., et al., Journal of Experimental Medicine, 167:175-182 (1988)), Der p II (Chua, K.Y., et al., International Archives of Allergy and Applied Immunology, 91:118-123 (1990)), Der f I (Dilworth, R.J., et al., Clinical and Experimental Allergy 21:25-32 (1991)), Der f II (Yuuki, T., et al., Japan

Journal Allergol., 39:557-461 (1990); and Trudinger, M., et al., Clinical and Experimental Allergy, 21:33-37 (1991)) and a low molecular weight allergen (Ovey, E.R., et al., Journal of Experimental Medicine, 170:1457-1462 (1989)).

The published nucleotide sequences of cDNAs encoding Der p I and Der f I demonstrate that these two proteins are highly homologous at the amino acid level (81% identity) and that the mature protein products are comprised of 222 and 223 residues, respectively (Chua, K.Y., et al., Journal of Experimental Medicine, 167:175-182 (1988); and Dilworth, R.J., et al., supra). The protein allergens Der p II and Der f II are both comprised of 129 residues, and are also highly homologous (88% identity) in amino acid sequence (Trudinger, M., et al. supra; Yuuki, T., et al. supra); Chua, K.Y., et al., International Archives of Allergy and Applied Immunology 91:118-123 (1990)).

The isolation of cDNAs clones encoding Der p I and Der p II has permitted antibody binding studies on the recombinant antigens (Green, W.K., et al., International Archives of Allergy and Applied Immunology, 92:30-38 (1990); Chua, K.Y., et al., International Archives of Allergy and Applied Immunology, 91:124-129 (1990)). Complementary DNA fragments of Der p I have been expressed in E. coli and IgE binding studies with pooled human mite allergic IgE sera have demonstrated binding and non-binding regions throughout the molecule (Thomas, W.R., et al., In: Epitopes of Atopic Allergens. Proceedings of Workshop from XIV Congress of the European Academy of Allergy and Clinical Immunology, Berlin, Sept. 1989. pp 77-82). T cell epitopes of Der p I have been reported (O'Hehir, R.E., et al., Annual Review Immunology, 9:67-95 (1991); Stewart, G.A., et al., In: Epitopes of Atopic Allergens. Proceedings of Workshop from XIV Congress of the European Academy of Allergy and Clinical Immunology, Berlin, Sept. 1989. pp 41-47; Yessel, H., et al., In: T cell Activation in Health and Disease: Discrimination Between Immunity and Tolerance, Conference 22-26 Sept., 1990, Trinity College, Oxford, U.K. and Hessel, H., et al., Journal of Immunology, 148 (3): 738-745 (Feb. 1, 1992).

### Summary of the Invention

The present invention provides isolated peptides of the major protein allergens of the genus Dermatophagoides. Peptides within the scope of the invention comprise at least one T cell epitope, preferably at least two T cell epitopes of a protein allergen selected from the allergens Der p I, Der p II, Der



f I, or Der f II. The invention further provides peptides comprising at least two regions, each region comprising at least one T cell epitope of a mite protein allergen. The regions are derived from the same or from different protein allergens of the genus Dermatophagoides.

The invention also provides modified peptides having similar or enhanced therapeutic properties as the corresponding, naturally-occurring allergen or portion thereof, but having reduced side effects, as well as modified peptides having improved properties such as increased solubility and stability. Peptides of the invention are capable of modifying, in a house dust mite-sensitive individual to whom they are administered, the allergic response of the individual to a house dust mite allergen or an allergen immunologically cross-reactive with house dust mite allergen. Methods of treatment or of diagnosis of sensitivity to house dust mite in an individual and therapeutic compositions comprising one or more peptides of the invention are also provided.

#### **Brief Description of the Drawings**

Fig. 1 shows the subcloning and expression of Group I and Group II allergens from D. pteronyssinus and D. farinae.

Fig. 2a shows adaptors used in the expression of Der p I and Der f I and Fig. 2b shows primers for amplification of Der f II and Der p II and a Der f II mutagenesis primer.

Fig. 3 shows various peptides of desired lengths derived from the Der p I and Der p II protein allergens.

Fig. 4 shows various peptides of desired lengths derived from the Der f I and Der f II protein allergens.

Fig. 5 is a graphic representation depicting the responses of T cell lines from 33 patients primed in vitro to either purified native (N) or recombinant (R) Der p I protein and analyzed for response to various overlapping Der p I peptides by percent of responses with a T cell Stimulation Index (S.I.) of at least 2 within the individuals tested, the mean T cell stimulation index of positive responses for the peptide and the ranked sum of peptide responses.

Fig. 6 is a graphic representation depicting the responses of T cell lines from 16 patients primed in vitro to the Der f I protein and analyzed for response to various overlapping Der f I peptides by percent of responses with an (S.I.) of at least 2 within the individuals tested, the mean T cell stimulation index of positive responses for the peptide and the ranked sum of peptide

responses.

Fig. 7 is a graphic representation depicting the responses of T cell lines from 14 patients primed in vitro to the Der p I protein and analyzed for response to various overlapping Der p I peptides and substantially matching Der f I peptides by percent of responses with an S.I. of at least 2 within the individuals tested, the mean T cell stimulation index of positive responses for the peptide and the ranked sum of peptide responses.

Fig. 8 is a graphic representation depicting the responses of T cell lines from 8 patients primed in vitro to the Der f I protein and analyzed for response to various overlapping Der f I peptides and substantially matching Der p I peptides by percent of responses with an S.I. of at least 2 within the individuals tested, the mean T cell stimulation index of positive responses for the peptide and the ranked sum of peptide responses.

Fig. 9 is a graphic representation depicting the responses of T cell lines from 29 patients primed in vitro to the Der p II protein and analyzed for response to various overlapping Der p II peptides by percent of responses with an S.I. of at least 2 within the individuals tested, the mean T cell stimulation index of positive responses for the peptide and the ranked sum of peptide responses.

Fig. 10 is a graphic representation depicting the responses of T cell lines from 10 patients primed in vitro to the Der f II protein and analyzed for response to various overlapping Der f II peptides by percent of responses with an S.I. of at least 2 within the individuals tested, the mean T cell stimulation index of positive responses for the peptide and the ranked sum of peptide responses.

Fig. 11 is a graphic representation depicting the responses of T cell lines from 10 patients primed in vitro to the Der f II protein and analyzed for response to various overlapping Der f II peptides and substantially matching Der p II peptides by percent of responses with an S.I. of at least 2 within the individuals tested, the mean T cell stimulation index of positive responses for the peptide and the ranked sum of peptide responses.

Fig. 12 is a graphic representation depicting the responses of T cell lines from 26 patients primed in vitro to the Der p II protein and analyzed for response to various overlapping Der f II peptides by percent of responses with an S.I. of at least 2 within the individuals tested, the mean T cell stimulation index of positive responses for the peptide and the ranked sum of peptide responses.

Fig. 13 is a graphic representation depicting the responses of T cell lines from 33 patients primed *in vitro* to the Der p I protein and analyzed for response to selected peptides of desired lengths derived from the Der p I protein allergen by percent of responses with an S.I. of at least 2 within the individuals tested, the mean T cell stimulation index of positive responses for the peptide and the ranked sum of peptide responses.

Fig. 14 is a graphic representation depicting the responses of T cell lines from 9 patients primed *in vitro* to the Der f I protein and analyzed for response to selected peptides of desired lengths derived from the Der f I protein allergen, by percent of responses with an S.I. of at least 2 within the individuals tested and the mean T cell stimulation index of positive responses for the peptide and the ranked sum of peptide responses.

Fig. 15a is a graphic representation depicting the responses of T cell lines from 30 matched patients primed *in vitro* to the Der p I protein and analyzed for response to selected peptides of desired lengths derived from the Der p I and the Der f I protein allergens, by percent of responses with an S.I. of at least 2 within the individuals tested and the mean T cell stimulation index of positive responses for the peptide.

Fig. 15b is a graphic representation derived from the same data shown in Fig. 15a showing the response of Der p I primed T cells to preferred Der p I peptides analyzed by percent of response with an S.I. of at least two within the individuals tested (above each bar), the mean T cell stimulation index (above each bar in parenthesis) and the ranked sum of peptide responses.

Fig. 16a is a graphic representation depicting the responses of T cell lines from 9 patients primed *in vitro* to the Der f I protein and analyzed for response to selected peptides of desired lengths derived from the Der f I and Der p I protein allergens, by percent of responses with an S.I. of at least 2 within the individuals tested and the mean T cell stimulation index of responses with an S.I. of at least 2 for the peptide.

Fig. 16b is a graphic representation derived from the same data shown in Fig. 16a showing the response of Der p I primed T cell lines to preferred Der f I and Der p I peptides by percent of responses with an S.I. of at least 2 within the individuals tested and the mean T cell stimulation index of responses with an S.I. of at least 2 for the peptide.

Fig. 17a is a graphic representation depicting the response of T cells from 29 patients primed *in vitro* to the Der p II protein and analyzed for response to selected peptides of desired lengths derived from the Der p II

protein, by the T cell stimulation index of a response with an S.I. of at least 2 for the peptide.

Fig. 17b is a graphic representation depicting the response of 30 patients primed in vitro to the Der p II protein and analyzed for response to selected peptides derived from the Der p II protein by percent of responses with an S.I. of at least 2 within the individuals tested (above each bar), the mean T cell stimulation index (above each bar in parenthesis) and the ranked sum of peptide response (X-axis).

Fig. 18a is a graphic representation depicting the response of T cells from 10 patients primed in vitro to the Der f II protein and analyzed for response to selected peptides of desired lengths derived from the Der p II and Der f II protein, by the T cell stimulation index of a response with an S.I. of at least 2 for the peptide.

Fig. 18b is a graphic representation derived from the same data shown in Fig. 18a showing the response of Der f II primed T cell lines to preferred Der p II peptides analyzed by percent responses with an S.I. of at least 2 within the individuals tested (above each bar), the mean T cell stimulation index (above each bar in parenthesis) and the ranked sum of peptide responses (X-axis).

Fig. 18c is a graphic representation depicting the responses of T cell lines from 4 matched patients primed in vitro with mite group I allergen and analyzed for response to preferred Der p I and Der f I peptides by percent of responses with an S.I. of at least 2 within the individuals tested and the mean T cell stimulation index of positive responses for the peptide.

Fig. 18d is a graphic representation depicting the responses of T cell lines from 6 matched patients primed in vitro with mite group II allergen and analyzed for response to preferred Der p II peptides by percent of responses with an S.I. of at least 2 within the individuals tested and the mean stimulation index of positive responses for the peptide.

Fig. 19a-19b are graphic representations of the results of a direct binding assay of IgE to affinity purified and recombinant Der p I and Der p II proteins and certain Der p I and Der p II overlapping peptides.

Fig. 20a-20b are graphic representations of the results of a direct binding assay of IgE to affinity purified and recombinant Der f I and Der f II proteins and certain Der f I and Der f II overlapping peptides.

Fig. 21a-21h are graphic representations of the results of a direct binding assay of IgE to a mixture of biochemically purified mite allergens (PMA)

and various peptides derived from Der p I, Der f I, Der p II and Der f II.

Fig. 22 is a composite alignment of the amino acid sequences of five Der p I clones (a)-(e) which illustrates polymorphism in the Der p I protein. The numbering refers to the sequence of the Der p I(a) clone. The symbol (-) is used to indicate that the amino acid residue of a Der p I clone is identical to the corresponding amino acid sequences of Der p I(a) at that position. The amino acid sequences of these clones indicate that there may be significant variation in Der p I, with five polymorphic amino acid residues found in the five sequences.

Fig. 23 is a composite alignment of the amino acid sequences of three Der p II clones (c), (1) and (2) which illustrates polymorphism in the Der p II protein. The numbering refers to the sequence of the Der p II(c) clone. The symbol (.) is used to indicate that the amino acid residue of a Der p II clone is identical to the corresponding amino acid residue of Der p II (c) at that position.

Fig. 24 is a composite alignment of the amino acid sequences of six Der f II clones (i.e., pFL1, pFL2, MT3, MT5, MT18 and MT16) which illustrates polymorphism in the Der f II protein. The numbering refers to the sequences of the Der f pLF1 clone. The symbol (.) is used to indicate that the amino acid residue of a Der f II clone is identical to the corresponding amino acid residue of Der f II pFL1 at that position.

Fig. 25 shows the nucleotide and amino acid sequences of a selected peptide which comprises various regions derived from Der p I, Der p II and Der f I protein allergens.

Fig. 26 shows the nucleotide and amino acid sequences of a selected peptide which comprises various regions derived from Der p I, Der p II and Der f I protein allergens.

Fig. 27 shows the nucleotide and amino acid sequences of a selected peptide which comprises various regions derived from Der p I, Der p II and Der f I protein allergens.

Fig. 28 shows the amino acid sequences of modified peptides in accordance with the invention.

### **Detailed Description of the Invention**

The present invention provides isolated peptides derived from the major protein allergens of the genus Dermatophagoides. As used herein, a peptide or fragment of a protein refers to an amino acid sequence having fewer amino acid residues than the entire amino acid sequence of the protein. Peptides of the invention include peptides derived from Der p I (SEQ ID NO: 1 and 2), Der p II

(SEQ ID NO: 3 and 4), Der f I (SEQ ID NO: 5 and 6) and Der f II (SEQ ID NO: 7 and 8) which comprise at least one T cell epitope of the allergen.

Peptides comprising at least two regions, each region comprising at least one T cell epitope of a protein allergen of the genus Dermatophagoides are also within the scope of the invention. Each region of such peptides is derived from the same or from different mite allergens. Isolated peptides or regions of isolated peptides, each comprising at least two T cell epitopes of a mite protein allergen are particularly desirable for increased therapeutic effectiveness. Peptides which are immunologically related (e.g., by antibody or T cell cross-reactivity) to peptides of the present invention are also within the scope of the invention. Peptides immunologically related by antibody cross-reactivity are bound by antibodies specific for a peptide of a protein allergen of the genus Dermatophagoides. Peptides immunologically related by T cell cross-reactivity are capable of reacting with the same T cells as a peptide of the invention.

Isolated peptides of the invention can be produced by recombinant DNA techniques in a host cell transformed with a nucleic acid having a sequence encoding such peptide. The isolated peptides of the invention can also be produced by chemical synthesis. In certain limited situations, isolated peptides can be produced by chemical cleavage of the protein allergen. When a peptide is produced by recombinant techniques, host cells transformed with a nucleic acid having a sequence encoding the peptide or the functional equivalent of the nucleic acid sequence are cultured in a medium suitable for the cells and peptides can be purified from cell culture medium, host cells, or both using techniques known in the art for purifying peptides and proteins including ion-exchange chromatography, gel filtration chromatography, ultrafiltration, electrophoresis or immunopurification with antibodies specific for the peptide, the protein allergen of the genus Dermatophagoides from which the peptide is derived, or a portion thereof. Isolated peptides of the invention are substantially free of cellular material or culture medium when produced by recombinant DNA techniques, or substantially free of chemical precursors or other chemicals when synthesized chemically.

The present invention provides expression vectors and host cells transformed to express the nucleic acid sequences of the invention. A nucleic acid sequence coding for a mite allergen, or at least one fragment thereof may be expressed in bacterial cells such as *E. coli*, insect cells (baculovirus), yeast, or mammalian cells such as Chinese hamster ovary cells (CHO). Suitable expression vectors, promoters, enhancers, and other expression control elements may be found in Sambrook et al. *Molecular Cloning: A Laboratory Manual*, second edition, Cold Spring Harbor

Laboratory Press, Cold Spring Harbor, New York (1989). Other suitable expression vectors, promoters, enhancers, and other expression elements are known to those skilled in the art. Expression in mammalian, yeast or insect cells leads to partial or complete glycosylation of the recombinant material and formation of any inter- or intra-chain disulfide bonds. Suitable vectors for expression in yeast include YepSec1 (Baldari et al. (1987) *Embo J.* 6: 229-234); pMFa (Kurjan and Herskowitz (1982) *Cell* 30: 933-943); JRY88 (Schultz et al. (1987) *Gene* 54: 113-123) and pYES2 (Invitrogen Corporation, San Diego, CA). These vectors are freely available. Baculovirus and mammalian expression systems are also available. For example, a baculovirus system is commercially available (PharMingen, San Diego, CA) for expression in insect cells while the pMSG vector is commercially available (Pharmacia, Piscataway, NJ) for expression in mammalian cells.

For expression in *E. coli*, suitable expression vectors include, among others, pTRC (Amann et al. (1988) *Gene* 69: 301-315); pGEX (Amrad Corp., Melbourne, Australia); pMAL (N.E. Biolabs, Beverly, MA); pRIT5 (Pharmacia, Piscataway, NJ); pET-11d (Novagen, Madison, WI) Jameel et al., (1990) *J. Virol.* 64:3963-3966; and pSEM (Knapp et al. (1990) *BioTechniques* 8: 280-281). The use of pTRC, and pET-11d, for example, will lead to the expression of unfused protein. The use of pMAL, pRIT5 pSEM and pGEX will lead to the expression of allergen fused to maltose E binding protein (pMAL), protein A (pRIT5), truncated  $\beta$ -galactosidase (PSEM), or glutathione S-transferase (pGEX). When a mite protein allergen, fragment, or fragments thereof is expressed as a fusion protein, it is particularly advantageous to introduce an enzymatic cleavage site at the fusion junction between the carrier protein and a mite protein allergen or fragment thereof. A mite protein allergen or fragment thereof may then be recovered from the fusion protein through enzymatic cleavage at the enzymatic site and biochemical purification using conventional techniques for purification of proteins and peptides. Suitable enzymatic cleavage sites include those for blood clotting Factor Xa or thrombin for which the appropriate enzymes and protocols for cleavage are commercially available from, for example, Sigma Chemical Company, St. Louis, MO and N.E. Biolabs, Beverly, MA. The different vectors also have different promoter regions allowing constitutive or inducible expression with, for example, IPTG induction (PRTC, Amann et al., (1988) *supra*; pET-11d, Novagen, Madison, WI) or temperature induction (pRIT5, Pharmacia, Piscataway, NJ).

To obtain isolated peptides of the present invention, a mite allergen is divided into non-overlapping peptides of desired length or overlapping peptides of desired lengths as discussed in Example III which can be produced recombinantly,

synthetically, or in certain limited situations, by chemical cleavage of the allergen. Peptides comprising at least one T cell epitope are capable of eliciting a T cell response, such as stimulation (i.e. proliferation or lymphokine secretion) and/or are capable of inducing T cell anergy (i.e., tolerization). To determine peptides comprising at least one T cell epitope, isolated peptides are tested by, for example, T cell biology techniques, to determine whether the peptides elicit a T cell response or induce T cell anergy. Those peptides found to elicit a T cell response or induce T cell anergy are defined as having T cell stimulating activity.

As discussed in the Examples, human T cell stimulating activity can be tested by culturing T cells obtained from an individual sensitive to a mite allergen, (i.e., an individual who has an IgE mediated immune response to a mite allergen) with a peptide derived from the allergen and determining whether proliferation of T cells occurs in response to the peptide as measured, e.g., by cellular uptake of tritiated thymidine. Stimulation indices for responses by T cells to peptides can be calculated as the maximum CPM in response to a peptide divided by the control CPM. A T cell stimulation index (S.I.) equal to or greater than two times the background level is considered "positive." Positive results are used to calculate the mean stimulation index for each peptide for the group of peptides tested. Preferred peptides of this invention comprise at least one T cell epitope and have a mean T cell stimulation index of greater than or equal to 2.0. A peptide having a T cell stimulation index of greater than or equal to 2.0 is considered useful as a therapeutic agent. Preferred peptides have a mean T cell stimulation index of at least 2.5, more preferably at least 3.5, even more preferably at least 4.0, and most preferably at least 5.0.

In addition, preferred peptides have a positivity index (P.I.) of at least about 100, more preferably at least 150, even more preferably at least about 200 and most preferably at least about 250. The positivity index for a peptide is determined by multiplying the mean T cell stimulation index by the percent of individuals, in a population of individuals sensitive to house dust mite (e.g., preferably at least 9 individuals, more preferably at least 16 individuals or more, more preferably at least 29 individuals or more, or even more preferably at least 30 individuals or more), who have T cells that respond to the peptide. Thus, the positivity index represents both the strength of a T cell response to a peptide (S.I.) and the frequency of a T cell response to a peptide in a population of individuals sensitive to house dust mite. For example, as shown in Fig. 5, peptide DP I-1 has a mean S.I. of 4.7 and 73% of positive responses in the group of individuals tested resulting in a positivity index of 343.1. Peptides of Der p I having a positivity index of at least about 150 and a mean



T cell stimulation index of at least about 4 include: DP I-1 (SEQ ID NO: 9); DP I-21.1 (SEQ ID NO: 27); DP I-21.2 (SEQ ID NO: 28); DP I-23.1 (SEQ ID NO: 33); DP I-23.2 (SEQ ID NO: 34); DP I-25.2 (SEQ ID NO: 36); and DP I-26.1 (SEQ ID NO: 37).

In order to determine precise T cell epitopes by, for example, fine mapping techniques, a peptide having T cell stimulating activity and thus comprising at least one T cell epitope as determined by T cell biology techniques is modified by addition or deletion of amino acid residues at either the amino or carboxy terminus of the peptide and tested to determine a change in T cell reactivity to the modified peptide. If two or more peptides which share an area of overlap in the native protein sequence are found to have human T cell stimulating activity, as determined by T cell biology techniques, additional peptides can be produced comprising all or a portion of such peptides and these additional peptides can be tested by a similar procedure. Following this technique, peptides are selected and produced recombinantly or synthetically. Peptides are selected based on various factors, including the strength of the T cell response to the peptide (e.g., stimulation index), the frequency of the T cell response to the peptide in a population of individuals sensitive to house dust mite, and the potential cross-reactivity of the peptide with other allergens of the genus Dermatophagoides. The physical and chemical properties of these selected peptides (e.g., solubility, stability) are examined to determine whether the peptides are suitable for use in therapeutic compositions or whether the peptides require modification as described herein. The ability of the selected peptides or selected modified peptides to stimulate human T cells (e.g., induce proliferation, lymphokine secretion) is determined.

Additionally, preferred peptides of the invention do not bind immunoglobulin E (IgE) or bind IgE to a substantially lesser extent than the protein allergen from which the peptide is derived binds IgE. The major complications of standard immunotherapy are IgE-mediated responses such as anaphylaxis. Immunoglobulin E is a mediator of anaphylactic reactions which result from the binding and cross-linking of antigen to IgE on mast cells or basophils and the release of mediators (e.g., histamine, serotonin, eosinophil chemotactic factors). Thus, anaphylaxis in a substantial percentage of a population of individuals sensitive to house dust mite could be avoided by the use in immunotherapy of a peptide or peptides which do not bind IgE in a substantial percentage (e.g., at least about 75%) of a population of individuals sensitive to a house dust mite allergen, or if the peptide binds IgE, such binding does not result in the release of mediators from mast cells or basophils. The risk of anaphylaxis could be reduced by the use in immunotherapy of a peptide or

peptides which have reduced IgE binding. Moreover, peptides which have minimal IgE stimulating activity are desirable for therapeutic effectiveness. Minimal IgE stimulating activity refers to IgE production that is less than the amount of IgE production and/or IL-4 production stimulated by the native protein allergen (e.g., Der p I).

A peptide of the invention, when administered to a house-dust mite-sensitive individual, is capable of modifying the allergic response of the individual to the allergen. Particularly, peptides of the invention comprising at least one T cell epitope of a mite allergen or at least two regions derived from a mite allergen, each comprising at least one T cell epitope, when administered to an individual sensitive to house dust mite are capable of modifying T cell response of the individual to the allergen. As used herein, modification of the allergic response of an individual to a house dust mite allergen can be defined as non-responsiveness or diminution in symptoms upon exposure to a mite allergen, as determined by standard clinical procedures (see e.g., Varney et al., British Medical Journal 302: 265-269 (1990)) including diminution in mite protein allergen induced asthmatic symptoms. As referred to herein, a diminution in symptoms includes any reduction in allergic response of an individual to the allergen after the individual has completed a treatment regimen with a peptide or protein of the invention. This diminution may be subjective (i.e. the patient feels more comfortable in the presence of the allergen). Diminution in symptoms can be determined clinically as well, using standard skin tests as is known in the art.

As a result of the work described herein, peptides derived from mite allergens comprising at least one T cell epitope have been produced. T cell epitopes are believed to be involved in initiation and perpetuation of the immune responses to mite allergen(s) which are responsible for the clinical symptoms of mite allergy. These T cell epitopes are thought to trigger early events at the level of the T helper cell by binding to an appropriate HLA molecule on the surface of an antigen presenting cell and stimulating the relevant T cell subpopulation. These events lead to T cell proliferation, lymphokine secretion, local inflammatory reactions, the recruitment of additional immune cells to the site, and activation of the B cell cascade leading to production of antibodies. One isotype of these antibodies, IgE, is fundamentally important in the development of allergic symptoms and its production is influenced early in the cascade of events, at the level of the T helper cell, by the nature of the lymphokines secreted. A T cell epitope is the basic element or smallest unit of recognition by a T cell receptor where the epitope comprises amino acid residues essential to receptor recognition which may be

contiguous and/or non-contiguous in the amino acid sequence of the protein. Amino acid sequences which mimic those of T cell epitopes and which modify the allergic response to protein allergens of the genus Der matophagoides are within the scope of this invention.

Exposure of mite allergic patients to peptides of the present invention may tolerize or anergize appropriate T cell subpopulations such that they become unresponsive to mite allergen(s) and do not participate in mounting an immune response upon such exposure. In addition, administration of a peptide of the present invention may modify the lymphokine secretion profile as compared with exposure to the naturally-occurring mite protein allergen or portion thereof (e.g., result in a decrease of IL-4 and/or an increase in IL-2). Furthermore, exposure to a peptide of the invention may influence T cell subpopulations which normally participate in the response to mite allergen(s) such that these T cells are drawn away from the site(s) of normal exposure to the allergen (e.g., nasal mucosa, skin, and lung) towards the site(s) of therapeutic administration of the peptide. This redistribution of T cell subpopulations may ameliorate or reduce the ability of an individual's immune system to mount an immune response at the site of normal exposure to the mite allergen(s), resulting in a diminution in allergic symptoms.

Isolated peptides of the invention comprise at least one T cell epitope of a protein allergen of the genus Dermatophagoides and accordingly, the peptide comprises at least approximately seven amino acid residues of the protein allergen. For purposes of therapeutic effectiveness, therapeutic compositions of the invention preferably comprise at least two T cell epitopes of a mite allergen. Accordingly, isolated peptides of the invention preferably comprise at least two T cell epitopes and accordingly, the peptide comprises at least approximately eight amino acid residues, and preferably fifteen amino acid residues. Additionally, therapeutic compositions of the invention preferably comprise a sufficient percentage of the T cell epitopes of the entire protein allergen such that a therapeutic regimen of administration of the composition to an individual sensitive to house dust mite, results in T cells of the individual being tolerized to the protein allergen. Synthetically produced peptides of the invention comprising up to approximately forty-five amino acid residues in length, and most preferably up to approximately thirty amino acid residues in length are particularly desirable as increases in length may result in difficulty in peptide synthesis as well as retention of an undesirable property (e.g., immunoglobulin binding or enzymatic activity) due to maintenance of conformational similarity between the peptide and the protein allergen from which it is derived. All of the peptides shown in Fig. 3 and Fig. 4 were found to

have human T cell stimulating activity.

Preferred peptides comprise all or a portion of the areas of major T cell reactivity within the Der p I, Der f I, Der p II and Der f II protein allergens, i.e., Region 1, Region 2, Region 3, Region 4, Region 5, Region 6a, Region 6b, Region 7, Region 8, Region 9 and Region 10. Each area is defined as follows: Region 1 comprises amino acid residues 1-28 of the Der p I and Der f I protein allergens; Region 2 comprises amino acid residues 36-68 of the Der p I and Der f I protein allergens; Region 3 comprises amino acid residues 74-109 of the Der p I and Der f I protein allergens; Region 4 comprises amino acid residues 118-139 of the Der p I and Der f I protein allergens; Region 5 comprises amino acid residues 141-166 of the Der p I and Der f I protein allergens; Region 6a comprises amino acid residues 161-185 of the Der p I and Der f I protein allergens; Region 6b comprises amino acid residues 173-201 of the Der p I and Der f I allergens; Region 7 comprises amino acid residues 1-26 of the Der p II and Der f II protein allergens; Region 8 comprises amino acid residues 33-67 of the Der p II and Der f II protein allergens; Region 9 comprises amino acid residues 79-104 of the Der p II and Der f II protein allergens and Region 10 comprises amino acid residues 107-129 of the Der p II and Der f II protein allergens.

Preferred peptides derived from the Der p I protein comprise all or a portion of the following peptides: DP I-1 (SEQ ID NO: 9); DP I-2 (SEQ ID NO: 10); DP I-3 (SEQ ID NO: 11); DP I-4 (SEQ ID NO: 12); DP I-11.1 (SEQ ID NO: 13); DP I-12.1 (SEQ ID NO: 14); DP I-5 (SEQ ID NO: 15); DP I-13 (SEQ ID NO: 17); DP I-14 (SEQ ID NO: 18); DP I-15 (SEQ ID NO: 19); DP I-6.1 (SEQ ID NO: 20); DP I-7.1 (SEQ ID NO: 21); DP I-8 (SEQ ID NO: 22); DP I-9 (SEQ ID NO: 23); DP I-16 (SEQ ID NO: 24); DP I-10 (SEQ ID NO: 25); DP I-17 (SEQ ID NO: 26); DP I-21.1 (SEQ ID NO: 27); DP I-21.2 (SEQ ID NO: 28); DP I-22.1 (SEQ ID NO: 29); DP I-22.2 (SEQ ID NO: 30); DP I-22.3 (SEQ ID NO: 31); DP I-22.4 (SEQ ID NO: 32); DP I-23.1 (SEQ ID NO: 33); DP I-23.2 (SEQ ID NO: 34); DP I-25.1 (SEQ ID NO: 35); DP I-25.2 (SEQ ID NO: 36); DP I-26.1 (SEQ ID NO: 37); DP I-27.1 (SEQ ID NO: 38); DP I-28.1 (SEQ ID NO: 39); and DP I-28.2 (SEQ ID NO: 40), wherein the portion of the peptide has a mean T cell stimulation index substantially equivalent to, or greater than the mean T cell stimulation index of the peptide from which it is derived as shown in Fig. 5 and Fig. 13. More preferably, peptides derived from the Der p I protein comprise all or a portion of the following peptides: DP I-21.2, DP I-22.2, DP I-23.1, DP I-25.2, DP I-26.1, DP I-27.1 and DP I-28.1, and most preferably, peptides derived from the Der p I protein comprises all or a portion of DP I-21.2, DP I-23.1 and DP I-26.1, wherein the portion of the peptide

has a mean T cell stimulation index substantially equivalent to, or greater than the mean T cell stimulation index of the peptide from which it is derived as shown in Fig. 5 and Fig. 13.

Preferred peptides derived from the Der f I, the Der p II and the Der f II proteins include: DF I-1 (SEQ ID NO: 72); DF I-2.1 (SEQ ID NO: 73); DF I-3 (SEQ ID NO: 74); DF I-4 (SEQ ID NO: 75); DF I-11 (SEQ ID NO: 76); DF I-12 (SEQ ID NO: 77); DF I-5 (SEQ ID NO: 78); DF I-13 (SEQ ID NO: 79); DF I-14 (SEQ ID NO: 80); DF I-15 (SEQ ID NO: 81); DF I-6 (SEQ ID NO: 82); DF I-7 (SEQ ID NO: 83); DF I-8.1 (SEQ ID NO: 84); DF I-8 (SEQ ID NO: 85); DF I-9 (SEQ ID NO: 86); DF I-16 (SEQ ID NO: 87); DF I-10 (SEQ ID NO: 88); DF I-17 (SEQ ID NO: 89); DF I-21.1 (SEQ ID NO: 90); DF I-21.2 (SEQ ID NO: 91); DF I-22.1 (SEQ ID NO: 92); DF I-22.2 (SEQ ID NO: 93); DF I-22.4 (SEQ ID NO: 94); DF I-23.1 (SEQ ID NO: 95); DF I-23.2 (SEQ ID NO: 96); DF I-25.1 (SEQ ID NO: 97); DF I-25.2 (SEQ ID NO: 98); DF I-26.1 (SEQ ID NO: 99); DF I-27.1 (SEQ ID NO: 100); DF I-28.1 (SEQ ID NO: 101); DF I-28.2 (SEQ ID NO: 102); DP II-20 (SEQ ID NO: 50); DP II-20.1 (SEQ ID NO: 51); DP II-20.2 (SEQ ID NO: 52); DP II-20.3 (SEQ ID NO: 53); DP II-20.4 (SEQ ID NO: 54); DP II-20.5 (SEQ ID NO: 55); DP II-20.6 (SEQ ID NO: 56); DP II-1 (SEQ ID NO: 41); DP II-2 (SEQ ID NO: 42); DP II-3.1 (SEQ ID NO: 43); DP II-4 (SEQ ID NO: 44); DP II-5 (SEQ ID NO: 45); DP II-6 (SEQ ID NO: 46); DP II-7 (SEQ ID NO: 47); DP II-8 (SEQ ID NO: 48); DP II-9 (SEQ ID NO: 49); DP II-1.1 (SEQ ID NO: 57); DP II-1.2 (SEQ ID NO: 58); DP II-2.1 (SEQ ID NO: 59); DP II-2.2 (SEQ ID NO: 60); DP II-2.3 (SEQ ID NO: 61); DP II-21 (SEQ ID NO: 62); DP II-22 (SEQ ID NO: 63); DP II-26 (SEQ ID NO: 64); DP II-26.1 (SEQ ID NO: 65); DP II-23 (SEQ ID NO: 66); DP II-23.1 (SEQ ID NO: 67); DP II-24 (SEQ ID NO: 68); DP II-25 (SEQ ID NO: 69); DP II-25.1 (SEQ ID NO: 70); DP II-25.2 (SEQ ID NO: 71); DF II-1 (SEQ ID NO: 103); DF II-2 (SEQ ID NO: 104); DF II-13.1 (SEQ ID NO: 105); DF II-3.1 (SEQ ID NO: 106); DF II-4.5 (SEQ ID NO: 107); DF II-4.3 (SEQ ID NO: 108); DF II-15 (SEQ ID NO: 109); DF II-16 (SEQ ID NO: 110); DF II-17 (SEQ ID NO: 111); DF II-18 (SEQ ID NO: 112); DF II-19 (SEQ ID NO: 113); DF II-19.1 (SEQ ID NO: 114); DF II-21 (SEQ ID NO: 115); and DF II-22 (SEQ ID NO: 116), or portions of the peptides comprising at least one T cell epitope. Preferably, a portion of a peptide derived from Der f I, Der p II and Der f II has a mean T cell stimulation index equivalent to or greater than the mean T cell stimulation index of the peptide from which it is derived as shown in Fig. 10, Fig. 15a, Fig. 15b and Fig. 16. More preferably, peptides derived from the Der p II and Der f I proteins comprise all or a portion of the following peptides: DF I-22.2, DP II-20.6, DP II-

22, DP II-24 and DP II-25.2.

One embodiment of the present invention features a peptide of a protein allergen of the genus Dermatophagoides. The peptide or portion thereof comprises at least one T cell epitope of the protein allergen and has a formula  $X_n$ -Y- $Z_m$ .

According to the formula, Y is an amino acid sequence selected from the group consisting of: DF I-21.1 (SEQ ID NO: 90); DF I-21.2 (SEQ ID NO: 91); DF I-22.1 (SEQ ID NO: 92); DF I-22.2 (SEQ ID NO: 93); DF I-22.4 (SEQ ID NO: 94); DF I-23.1 (SEQ ID NO: 95); DF I-23.2 (SEQ ID NO: 96); DF I-25.1 (SEQ ID NO: 97); DF I-25.2 (SEQ ID NO: 98); DF I-26.1 (SEQ ID NO: 99); DF I-27.1 (SEQ ID NO: 100); DF I-28.1 (SEQ ID NO: 101); DF I-28.2 (SEQ ID NO: 102); DF I-1 (SEQ ID NO: 72); DP II-20 (SEQ ID NO: 50); DP II-20.1 (SEQ ID NO: 51); DP II-20.2 (SEQ ID NO: 52); DP II-20.3 (SEQ ID NO: 53); DP II-20.4 (SEQ ID NO: 54); DP II-20.5 (SEQ ID NO: 55); DP II-20.6 (SEQ ID NO: 56); DP II-1 (SEQ ID NO: 41); DP II-1.1 (SEQ ID NO: 57); DP II-1.2 (SEQ ID NO: 58); DP II-2.1 (SEQ ID NO: 59); DP II-2.2 (SEQ ID NO: 60); DP II-2.3 (SEQ ID NO: 61); DP II-21 (SEQ ID NO: 62); DP II-22 (SEQ ID NO: 63); DP II-26 (SEQ ID NO: 64); DP II-26.1 (SEQ ID NO: 65); DP II-23 (SEQ ID NO: 66); DP II-23.1 (SEQ ID NO: 67); DP II-24 (SEQ ID NO: 68); DP II-25 (SEQ ID NO: 69); DP II-25.1 (SEQ ID NO: 70); DP II-25.2 (SEQ ID NO: 71); DF II-1 (SEQ ID NO: 103); DF II-2 (SEQ ID NO: 104); DF II-13.1 (SEQ ID NO: 105); DF II-3.1 (SEQ ID NO: 106); DF II-4.5 (SEQ ID NO: 107); DF II-4.3 (SEQ ID NO: 108); DF II-15 (SEQ ID NO: 109); DF II-16 (SEQ ID NO: 110); DF II-17 (SEQ ID NO: 111); DF II-18 (SEQ ID NO: 112); DF II-19 (SEQ ID NO: 113); DF II-19.1 (SEQ ID NO: 114); DF II-21 (SEQ ID NO: 115); and DF II-22 (SEQ ID NO: 116). In addition,  $X_n$  are amino acid residues contiguous to the amino terminus of Y in the amino acid sequence of the protein allergen and  $Z_m$  are amino acid residues contiguous to the carboxy terminus of Y in the amino acid sequence of the protein allergen. In the formula, n is 0-30 and m is 0-30.

Another embodiment of the present invention provides peptides comprising at least two regions, each region comprising at least one T cell epitope of a protein allergen of the genus Dermatophagoides and accordingly, each region comprises at least approximately seven amino acid residues). These peptides comprising at least two regions can comprise as many amino acid residues as desired and preferably comprise at least about 14, even more preferably about 30, and most preferably at least about 40 amino acid residues of a mite allergen. Each region of such peptide preferably comprises up to 45 amino acid residues in length, more preferably up to 40 residues in length and most preferably up to 30 amino acid residues in length as

increases in length of a region may result in difficulty in peptide synthesis as well as retention of an undesirable property (e.g., immunoglobulin binding or enzymatic activity) due to maintenance of conformational similarity between the peptide and the protein allergen from which it is derived. If desired, the amino acid sequences of the regions can be produced and joined by a linker to increase sensitivity to processing by antigen-presenting cells. Such linker can be any non-epitope amino acid sequence or other appropriate linking or joining agent. To obtain preferred peptides comprising at least two regions, each comprising at least one T cell epitope, the regions are arranged in a configuration different from a naturally-occurring configuration of the regions in the allergen or a combination of different mite protein allergens. For example, the regions containing T cell epitope(s) can be arranged in a noncontiguous configuration and can preferably be derived from the same protein allergen or a combination of protein allergens. Noncontiguous is defined as an arrangement of regions containing T cell epitope(s) which is different than that of an amino acid sequence present in the protein allergen from which the regions are derived. Furthermore, the noncontiguous regions containing T cell epitopes can be arranged in a nonsequential order (e.g., in an order different from the order of the amino acids of the native protein allergen from which the region containing T cell epitope(s) are derived in which amino acids are arranged from an amino terminus to a carboxy terminus). A peptide can comprise at least 15%, at least 30%, at least 50% or up to 100% of the T cell epitopes of a mite allergen.

The individual peptide regions can be produced and tested to determine which regions bind immunoglobulin E specific for a mite allergen and which of such regions would cause the release of mediators (e.g., histamine) from mast cells or basophils. Those peptide regions found to bind immunoglobulin E and cause the release of mediators from mast cells or basophils in greater than approximately 10-15% of the allergic sera tested are preferably not included in the peptide regions arranged to form peptides of the invention.

Preferred peptides of the invention comprise two or more regions derived from the same or from different mite allergens (e.g. Der p I, Der p II, Der f I and Der f II). For example, one region can be derived from Der p I and one region can be derived from Der p II; one region can be derived from Der p I and one region can be derived from Der f I; one region can be derived from Der p II and one region can be derived from Der f I; one region can be derived from Der p II and one region can be derived from Der f II; one region can be derived from Der p I and one region can be derived from Der f II; and one region can be derived from Der f I and one region can be derived from Der f II. In addition, the regions can be

derived from the same protein allergen, e.g., Der p I and Der p I, etc.

Regions of a peptide of the invention preferably comprise all or a portion of the above discussed preferred areas of major T cell reactivity within each mite allergen (i.e., Regions 1-6a-6b of Der p I and Der f I and Regions 7-10 of Der p II and Der f II). For example, one region can comprise all or a portion of Region 1 (amino acid residues 1-28 of Der p I or Der f I) and one region can comprise all or a portion of Region 2 (amino acid residues 36-68 of Der p I or Der f I). Peptides of the invention can comprise all or a portion of two or more of these Regions (i.e., Regions 1-10) and preferred resulting peptides do not bind IgE and cause the release of mediators from mast cells or basophils. Preferred peptides derived from Der p I and Der f I comprise all or a portion of Region 1, Region 2, Region 3 and optionally Region 4. Preferred peptides derived from Der p II and Der f II comprise all or a portion of Region 7 and Region 8 and, Region 10. Further, if one of these Regions is found to bind IgE and cause the release of mediators from mast cells or basophils, then it is preferred that the peptide not comprise such Regions but rather comprises various Regions derived from such Regions which do not bind IgE or cause release of mediators from mast cells or basophils.

Examples of preferred regions include all or a portion of the following amino acid sequences: DP I-21.1 (SEQ ID NO: 27); DP I-21.2 (SEQ ID NO: 28); DP I-22.1 (SEQ ID NO: 29); DP I-22.2 (SEQ ID NO: 30); DP I-22.3 (SEQ ID NO: 31); DP I-22.4 (SEQ ID NO: 32); DP I-23.1 (SEQ ID NO: 33); DP I-23.2 (SEQ ID NO: 34); DP I-25.1 (SEQ ID NO: 35); DP I-25.2 (SEQ ID NO: 36); DP I-26.1 (SEQ ID NO: 37); DP I-27.1 (SEQ ID NO: 38); DP I-28.1 (SEQ ID NO: 39); DP I-28.2 (SEQ ID NO: 40); DP I-1 (SEQ ID NO: 9); DF I-1 (SEQ ID NO: 72); DF I-21.1 (SEQ ID NO: 90); DF I-21.2 (SEQ ID NO: 91); DF I-22.1 (SEQ ID NO: 92); DF I-22.2 (SEQ ID NO: 93); DF I-22.4 (SEQ ID NO: 94); DF I-23.1 (SEQ ID NO: 95); DF I-23.2 (SEQ ID NO: 96); DF I-25.1 (SEQ ID NO: 97); DF I-25.2 (SEQ ID NO: 98); DF I-26.1 (SEQ ID NO: 99); DF I-27.1 (SEQ ID NO: 100); DF I-28.1 (SEQ ID NO: 101); DF I-28.2 (SEQ ID NO: 102); DP II-20 (SEQ ID NO: 50); DP II-20.1 (SEQ ID NO: 51); DP II-20.2 (SEQ ID NO: 52); DP II-20.3 (SEQ ID NO: 53); DP II-20.4 (SEQ ID NO: 54); DP II-20.5 (SEQ ID NO: 55); DP II-20.6 (SEQ ID NO: 56); DP II-1 (SEQ ID NO: 41); DP II-1.1 (SEQ ID NO: 57); DP II-1.2 (SEQ ID NO: 58); DP II-2.1 (SEQ ID NO: 59); DP II-2.2 (SEQ ID NO: 60); DP II-2.3 (SEQ ID NO: 61); DP II-21 (SEQ ID NO: 62); DP II-22 (SEQ ID NO: 63); DP II-26 (SEQ ID NO: 64); DP II-26.1 (SEQ ID NO: 65); DP II-23 (SEQ ID NO: 66); DP II-23.1 (SEQ ID NO: 67); DP II-24 (SEQ ID NO: 68); DP II-25 (SEQ ID NO: 69); DP II-25.1 (SEQ ID NO: 70); DP II-25.2 (SEQ ID NO: 71); DF II-1 (SEQ ID



NO: 103) DF II-2 (SEQ ID NO: 104); DF II-13.1 (SEQ ID NO: 105); DF II-3.1 (SEQ ID NO: 106); DF II-4.5 (SEQ ID NO: 107); DF II-4.3 (SEQ ID NO: 108); DF II-15 (SEQ ID NO: 109); DF II-16 (SEQ ID NO: 110); DF II-17 (SEQ ID NO: 111); DF II-18 (SEQ ID NO: 112); DF II-19 (SEQ ID NO: 113); DF II-19.1 (SEQ ID NO: 114); DF II-21 (SEQ ID NO: 115); and DF II-22 (SEQ ID NO: 116), the amino acid sequences of such regions being shown in Fig. 3 and Fig. 4, or portions of said regions comprising at least one T cell epitope.

Preferred peptides comprise various combinations of two or more regions, each region comprising all or a portion of the above-discussed preferred areas of major T cell reactivity. Preferred peptides comprise a combination of two or more regions (each region having an amino acid sequence as shown in Fig. 3 and Fig. 4) including: DP I-22.1 (SEQ ID NO: 29) and DP I-25.1 (SEQ ID NO: 35); DP I-21.1 (SEQ ID NO: 27) and DP I-25.2 (SEQ ID NO: 36); DP I-22.1 (SEQ ID NO: 29) and DP I-1 (SEQ ID NO: 9); DP I-21.1 (SEQ ID NO: 27), DP I-22.1 (SEQ ID NO: 29), and DP I-25.2 (SEQ ID NO: 36); DP I-21.2 (SEQ ID NO: 28), DP I-22.1 (SEQ ID NO: 29), and DP I-23.1 (SEQ ID NO: 39); DP I-1 (SEQ ID NO: 9), DP I-22.1 (SEQ ID NO: 29), and DP I-23.1 (SEQ ID NO: 33); DP I-1 (SEQ ID NO: 9), DP I-22.1 (SEQ ID NO: 29), and DP I-25.2 (SEQ ID NO: 36); DP I-21.1 (SEQ ID NO: 27), DP I-22.1 (SEQ ID NO: 29), DP I-23.1 (SEQ ID NO: 33), and DP I-25.2 (SEQ ID NO: 36); DP I-21.2 (SEQ ID NO: 28), DP I-22.1 (SEQ ID NO: 29), and DP I-25.2 (SEQ ID NO: 36); DP I-21.2 (SEQ ID NO: 27), DP I-22.1 (SEQ ID NO: 29), DP I-25.2 (SEQ ID NO: 36), and DP I-26.1 (SEQ ID NO: 37); DF I-21.2 (SEQ ID NO: 91) and DF I-22.1 (SEQ ID NO: 92); DF I-21.1 (SEQ ID NO: 90), DF I-22.1 (SEQ ID NO: 92), and DF I-25.1 (SEQ ID NO: 97); DF I-21.2 (SEQ ID NO: 91), DF I-22.1 (SEQ ID NO: 92), and DF I-25.1 (SEQ ID NO: 97); DF I-1 (SEQ ID NO: 72) and DF I-22.1 (SEQ ID NO: 92); DF I-1 (SEQ ID NO: 72), DF I-22.1 (SEQ ID NO: 92), and DF I-25.1 (SEQ ID NO: 97); DF I-22.1 (SEQ ID NO: 29), and DF I-25.1 (SEQ ID NO: 35); DF I-21.1 (SEQ ID NO: 90), DF I-22.1 (SEQ ID NO: 92), and DF I-23.1 (SEQ ID NO: 95); DP I-21.1 (SEQ ID NO: 27), and DF I-22.1 (SEQ ID NO: 92); DP I-1 (SEQ ID NO: 9), DP I-23.1 (SEQ ID NO: 33), DP I-25.1 (SEQ ID NO: 35), and DF I-1 (SEQ ID NO: 72); t) DP I-1 (SEQ ID NO: 9), DP I-25.1 (SEQ ID NO: 35), DP I-23.1 (SEQ ID NO: 33), and DF I-21.2 (SEQ ID NO: 91); DP I-1 (SEQ ID NO: 9), DP I-25.1 (SEQ ID NO: 35), DP I-23.1 (SEQ ID NO: 33), and DF I-21.1 (SEQ ID NO: 90); DP II-22 (SEQ ID NO: 63), and DP II-25.2 (SEQ ID NO: 71); DP II-22 (SEQ ID NO: 63), DP II-25.2 (SEQ ID NO: 71), and DP I-21.1 (SEQ ID NO: 27) and DP I-22.1 (SEQ ID NO: 29); DP II-22 (SEQ ID NO: 63), DP II-25.2 (SEQ ID NO: 71), DP II-20.6 (SEQ ID

NO: 56), DP I-22.1 (SEQ ID NO: 29), DP I-21.1 (SEQ ID NO: 27), and DP I-23.1 (SEQ ID NO: 33); DP II-22 (SEQ ID NO: 63), DP II-25.2 (SEQ ID NO: 71), DP II-20.6 (SEQ ID NO: 56), DP I-21.1 (SEQ ID NO: 27), DP I-22.1 (SEQ ID NO: 29), and DP I-25.2 (SEQ ID NO: 36); DP II-22 (SEQ ID NO: 63), DP II-25.2 (SEQ ID NO: 71), DP I-21.1 (SEQ ID NO: 27), DP I-22.1 (SEQ ID NO: 29), and DP I-25.2 (SEQ ID NO: 36); DP II-22 (SEQ ID NO: 63), DP II-25.2 (SEQ ID NO: 71), DP I-21.1 (SEQ ID NO: 27), DP I-22.1 (SEQ ID NO: 29), and DP I-23.1 (SEQ ID NO: 33); DP II-22 (SEQ ID NO: 63), DP II-25.2 (SEQ ID NO: 71), DP I-1 (SEQ ID NO: 9), and DP I-22.1 (SEQ ID NO: 29); DF II-4.5 (SEQ ID NO: 107) and DF II-2 (SEQ ID NO: 104); DF II-4.5 (SEQ ID NO: 107) and DF II-19.1 (SEQ ID NO: 114); DF II-4.5 (SEQ ID NO: 107), DF II-2 (SEQ ID NO: 104), and DF II-19.1 (SEQ ID NO: 114); DF II-4.5 (SEQ ID NO: 107), DF II-2 (SEQ ID NO: 104), and DF II-9 (SEQ ID NO: 86); DF II-4.5 (SEQ ID NO: 107); and DF I-21.1 (SEQ ID NO: 90); DF II-4.5 (SEQ ID NO: 107), DP II-22 (SEQ ID NO: 63), and DP II-25.2 (SEQ ID NO: 71); and  
 i) DF II-4.5 (SEQ ID NO: 107), DF II-2 (SEQ ID NO: 104), and DP II-22 (SEQ ID NO: 63).

Additional preferred peptides comprising a combination of two or more Regions and including the following combinations: DP I-21.2, DP I-23.1, DP I-26.1, DP II-20.6, DP II-22, DP II-25.2 and DF II-22.2; DP I-21.2, DF II-22.2; DP I-21.2, DF I-22.2, DP I-23.1, DP I-25.2, DP I-26.1, DP I-27.1, DP II-20.6, DP II-22, DP II-24, and DP II-25.2; DP I-23.1, DP I-21.2, DP I-22, DF I-22.2, DP II-20.6, and DP II-25.2; DP I-23.1, DP I-21.2, DF I-22.2, DP II-20.6, and DP II-25.2; DP I-23.1, DF I-22 and DP II-20.6; DP I-26.1, DF I-22.2 and DP II-25.2; DP I-21.2, DF I-22.2 and DP II-22; and DP I-21.2 and DP II-22.

The most preferred peptides comprise a combination of two or more regions (each region having an amino acid sequence as shown in Fig. 3 and Fig. 4) derived from mite allergens Der p I, Der p II, and Der f I each of said preferred peptides having the following specific sequential arrangement of amino acid sequences as shown in Figs. 25-27: DPI-26.1, DPII-25.2, DFI-22, DPII-20.6 and DPI-21.2 respectively; DPII-25.2, DFI-22.2, DPI-23.1, DPII-22, DPI-21.2 and DPII-20.6 respectively; and DPII-25.2, DPI-21.2, DPI-23.1, DPI-26.1, DPII-22, DPII-20.6 and DFI-22.2 respectively. The nucleic acid and amino acid sequences of the above peptides are shown in Figs. 25, 26 and 27 respectively.

Peptides of protein allergens of the genus Dermatophagoides within the scope of the invention can be used in methods of treating and preventing allergic reactions to mite allergens. Thus, one aspect of the present invention

provides therapeutic compositions comprising a peptide of Der p I, Der p II, Der f I, or Der f II including at least one T cell epitope, or preferably at least two T cell epitopes, and a pharmaceutically acceptable carrier or diluent. In another aspect, the therapeutic composition comprises a pharmaceutically acceptable carrier or diluent and a peptide comprising at least two regions, each region comprising at least one T cell epitope of a mite allergen and derived from the same or from different mite protein allergens.

Preferred therapeutic compositions comprise at least one peptide of at least one protein allergen of the genus Dermatophagoides. The composition comprises a sufficient percentage of the T cell epitopes of at least one protein allergen such that a therapeutic regimen of administration of the composition to an individual sensitive to a house dust mite allergen resulting in T cells of the individual being tolerized to the protein allergen. Preferably, the composition comprises a sufficient percentage of the T cell epitopes of one or more protein allergens such that at least about 40%, and more preferably at least about 60% of the T cell reactivity of each protein is included in the composition. Such compositions can be administered to an individual to treat or prevent sensitivity to house dust mite or to an allergen which is immunologically cross-reactive with house dust mite.

Administration of the therapeutic compositions of the present invention to desensitize an individual can be carried out using known techniques. For example, a peptide derived from a mite allergen comprising at least one T cell epitope can be administered in combination with an appropriate diluent, a carrier, and/or an adjuvant. To induce T cell anergy in an individual, the therapeutic composition is preferably administered in non-immunogenic form, e.g. it does not contain adjuvant. Pharmaceutically acceptable diluents include saline and aqueous buffer solutions. Pharmaceutically acceptable carriers include polyethylene glycol (Wie et al. International Archives of Allergy and Applied Immunology 64: 84-99 (1981)) and liposomes (Strejan et al., Journal of Neuroimmunology 7: 27 (1984)). Such compositions will generally be administered by injection, (subcutaneous, intravenous, etc.) oral administration, (e.g. as in the form of a capsule), inhalation, transdermal application or rectal administration. The therapeutic compositions of the invention are administered to individuals sensitive to house dust mite at dosages and for lengths of time effective to reduce sensitivity (i.e., reduce the allergic response) of the individual to a house dust mite allergen. A therapeutically effective amount of one or more of the same or of different therapeutic compositions can be administered simultaneously or sequentially to an individual sensitive to house dust mite. Effective amounts of the therapeutic compositions will vary according to factors such

as the degree of sensitivity of the individual to house dust mites, the age, sex, and weight of the individual, and the ability of the peptide to stimulate a T cell response in the individual.

In yet another aspect of the present invention, a composition is provided comprising at least two peptides (e.g., a physical mixture of at least two peptides), each comprising at least one T cell epitope of a protein allergen of the genus Dermatophagoides. The peptides are derived from the same or from different mite allergens. Such compositions can be administered in the form of a therapeutic composition with a pharmaceutically acceptable carrier or diluent. A therapeutically effective amount of one or more of such compositions can be administered simultaneously or sequentially to an individual sensitive to house dust mite.

Preferred compositions and preferred combinations of peptides which can be administered simultaneously or sequentially (comprising peptides having amino acid sequences shown in Fig. 3 and Fig. 4) include the following combinations: DP I-22.1 (SEQ ID NO: 29) and DP I-25.1 (SEQ ID NO: 35); DP I-21.1 (SEQ ID NO: 27) and DP I-25.2 (SEQ ID NO: 36); DP I-22.1 (SEQ ID NO: 29) and DP I-1 (SEQ ID NO: 9); DP I-21.1 (SEQ ID NO: 27), DP I-22.1 (SEQ ID NO: 29), and DP I-25.2 (SEQ ID NO: 36); DP I-21.2 (SEQ ID NO: 28), DP I-22.1 (SEQ ID NO: 29), and DP I-23.1 (SEQ ID NO: 39); DP I-1 (SEQ ID NO: 9), DP I-22.1 (SEQ ID NO: 29), and DP I-23.1 (SEQ ID NO: 33); DP I-1 (SEQ ID NO: 9), DP I-22.1 (SEQ ID NO: 29), and DP I-25.2 (SEQ ID NO: 36); DP I-21.1 (SEQ ID NO: 27), DP I-22.1 (SEQ ID NO: 29), DP I-23.1 (SEQ ID NO: 33), and DP I-25.2 (SEQ ID NO: 36); DP I-21.2 (SEQ ID NO: 28), DP I-22.1 (SEQ ID NO: 29), and DP I-25.2 (SEQ ID NO: 36); DP I-21.2 (SEQ ID NO: 27), DP I-22.1 (SEQ ID NO: 29), DP I-25.2 (SEQ ID NO: 36), and DP I-26.1 (SEQ ID NO: 37); DF I-21.2 (SEQ ID NO: 91) and DF I-22.1 (SEQ ID NO: 92); DF I-21.1 (SEQ ID NO: 90), DF I-22.1 (SEQ ID NO: 92), and DF I-25.1 (SEQ ID NO: 97); DF I-21.2 (SEQ ID NO: 91), DF I-22.1 (SEQ ID NO: 92), and DF I-25.1 (SEQ ID NO: 97); DF I-1 (SEQ ID NO: 72) and DF I-22.1 (SEQ ID NO: 92); DF I-1 (SEQ ID NO: 72), DF I-22.1 (SEQ ID NO: 92), and DF I-25.1 (SEQ ID NO: 97); DF I-22.1 (SEQ ID NO: 29), and DF I-25.1 (SEQ ID NO: 35); DF I-21.1 (SEQ ID NO: 90), DF I-22.1 (SEQ ID NO: 92), and DF I-23.1 (SEQ ID NO: 95); DP I-21.1 (SEQ ID NO: 27), and DF I-22.1 (SEQ ID NO: 92); DP I-1 (SEQ ID NO: 9), DP I-23.1 (SEQ ID NO: 33), DP I-25.1 (SEQ ID NO: 35), and DF I-1 (SEQ ID NO: 72); DP I-1 (SEQ ID NO: 9), DP I-25.1 (SEQ ID NO: 35), DP I-23.1 (SEQ ID NO: 33), and DF I-21.2 (SEQ ID NO: 91); DP I-1 (SEQ ID NO: 9), DP I-25.1 (SEQ ID NO: 35), DP I-23.1 (SEQ ID NO: 33), and DF I-21.1 (SEQ ID NO: 90); DP II-22 (SEQ ID NO:

63), and DP II-25.2 (SEQ ID NO: 71); DP II-22 (SEQ ID NO: 63), DP II-25.2 (SEQ ID NO: 71), and DP I-21.1 (SEQ ID NO: 27) and DP I-22.1 (SEQ ID NO: 29); DP II-22 (SEQ ID NO: 63), DP II-25.2 (SEQ ID NO: 71), DP II-20.6 (SEQ ID NO: 56), DP I-22.1 (SEQ ID NO: 29), DP I-21.1 (SEQ ID NO: 27), and DP I-23.1 (SEQ ID NO: 33); DP II-22 (SEQ ID NO: 63), DP II-25.2 (SEQ ID NO: 71), DP II-20.6 (SEQ ID NO: 56), DP I-21.1 (SEQ ID NO: 27), DP I-22.1 (SEQ ID NO: 29), and DP I-25.2 (SEQ ID NO: 36); DP II-22 (SEQ ID NO: 63), DP II-25.2 (SEQ ID NO: 71), DP I-21.1 (SEQ ID NO: 27), DP I-22.1 (SEQ ID NO: 29), and DP I-25.2 (SEQ ID NO: 36); DP II-22 (SEQ ID NO: 63), DP II-25.2 (SEQ ID NO: 71), DP I-21.1 (SEQ ID NO: 27), DP I-22.1 (SEQ ID NO: 29), and DP I-23.1 (SEQ ID NO: 33); DP II-22 (SEQ ID NO: 63), DP II-25.2 (SEQ ID NO: 71), DP I-1 (SEQ ID NO: 9), and DP I-22.1 (SEQ ID NO: 29); DF II-4.5 (SEQ ID NO: 107) and DF II-2 (SEQ ID NO: 104); DF II-4.5 (SEQ ID NO: 107) and DF II-19.1 (SEQ ID NO: 114); DF II-4.5 (SEQ ID NO: 107), DF II-2 (SEQ ID NO: 104), and DF II-19.1 (SEQ ID NO: 114); DF II-4.5 (SEQ ID NO: 107), DF II-2 (SEQ ID NO: 104), and DF II-9 (SEQ ID NO: 86); DF II-4.5 (SEQ ID NO: 107); and DF I-21.1 (SEQ ID NO: 90); DF II-4.5 (SEQ ID NO: 107), DP II-22 (SEQ ID NO: 63), and DP II-25.2 (SEQ ID NO: 71); and DF II-4.5 (SEQ ID NO: 107), DF II-2 (SEQ ID NO: 104), and DP II-22 (SEQ ID NO: 63); and DP I-26.1, DP II-25.2, DF I-22, DP II-20.6 and DP I-21.2.

The present invention also provides methods of detecting sensitivity in individuals to house dust mite allergens comprising combining a blood sample obtained from the individual with a peptide of the present invention, under conditions appropriate for binding of blood components with the peptide and determining the extent to which such binding occurs. The extent to which binding occurs is determined by assessing T cell function, T cell proliferation or a combination thereof.

It is also possible to modify the structure of a peptide of the invention for such purposes as increasing solubility, enhancing therapeutic or preventive efficacy, or stability (e.g., shelf life *ex vivo*, and resistance to proteolytic degradation *in vivo*). A modified peptide can be produced in which the amino acid sequence has been altered, such as by amino acid substitution, deletion, or addition, to modify immunogenicity and/or reduce allergenicity, or to which a component has been added for the same purpose.

For example, a peptide can be modified so that it maintains the ability to induce T cell anergy and bind MHC proteins without the ability to induce a strong proliferative response or possibly, any proliferative response when

administered in immunogenic form. In this instance, critical binding residues for the T cell receptor can be determined using known techniques (e.g., substitution of each residue and determination of the presence or absence of T cell reactivity). Those residues shown to be essential to interact with the T cell receptor can be modified by replacing the essential amino acid with another, preferably similar amino acid residue (a conservative substitution) whose presence is shown to enhance, diminish but not eliminate, or not effect T cell reactivity. In addition, those amino acid residues which are not essential for T cell receptor interaction can be modified by being replaced by another amino acid whose incorporation may enhance, diminish or not effect T cell reactivity but does not eliminate binding to relevant MHC.

Additionally, peptides of the invention can be modified by replacing an amino acid shown to be essential to interact with the MHC protein complex with another, preferably similar amino acid residue (conservative substitution) whose presence is shown to enhance, diminish but not eliminate or not effect T cell activity. In addition, amino acid residues which are not essential for interaction with the MHC protein complex but which still bind the MHC protein complex can be modified by being replaced by another amino acid whose incorporation may enhance, not effect, or diminish but not eliminate T cell reactivity. Preferred amino acid substitutions for non-essential amino acids include, but are not limited to substitutions with alanine, glutamic acid, or a methyl amino acid.

Another example of a modification of peptides is substitution of cysteine residues preferably with serine, threonine, leucine or glutamic acid to minimize dimerization via disulfide linkages. For example, the stability of a peptide of Der p II or Der f II which includes the first ten amino acid residues of either allergen can be enhanced by replacing the cysteine located at the 8th amino acid residue, preferably with alanine, or glutamic acid, or alternatively with serine or threonine.

In order to enhance stability and/or reactivity, peptides can also be modified to incorporate one or more polymorphisms in the amino acid sequence of a protein allergen resulting from natural allelic variation as shown in Figs. 25-27. Additionally, D-amino acids, non-natural amino acids or non-amino acid analogues can be substituted or added to produce a modified peptide within the scope of this invention. Furthermore, peptides of the present invention can be modified using the polyethylene glycol (PEG) method of A. Schon and co-workers (Wie et al. supra) to produce a peptide conjugated with PEG. In addition,

PEG can be added during chemical synthesis of a peptide of the invention. Modifications of peptides or portions thereof can also include reduction/alkylation (Tarr in: Methods of Protein Microcharacterization, J.E. Silver ed. Humana Press, Clifton, NJ, pp 155-194 (1986)); acylation (Tarr, supra); esterification (Tarr, supra); chemical coupling to an appropriate carrier (Mishell and Shiigi, eds. Selected Methods in Cellular Immunology, WH Freeman, San Francisco, CA (1980); U.S. Patent 4,939,239); or mild formalin treatment (Marsh International Archives of Allergy and Applied Immunology 41: 199-215 (1971)).

In another embodiment, peptides within an allergen group (e.g., Der p I or Der p II) can be modified to enhance T cell reactivity. Given the cross-reactivity within the Group I and Group II allergens, a peptide of one group allergen which may be less reactive than a peptide of another group allergen corresponding in amino acid position can have one or more amino acids substituted with one or more amino acids from the corresponding peptide (e.g., peptide DF II-1, residue seventeen [methionine] in the Der f II amino acid sequence can be substituted with the amino acid located at residue seventeen in Der p II [leucine] to enhance the reactivity of the Der f II peptide). Additionally, peptides can be modified to incorporate a polymorphism in the amino acid sequence of a protein allergen resulting from natural allelic variation. Modification of peptides to include one or more of these polymorphisms may result in enhanced stability and/or reactivity.

To facilitate purification and potentially increase solubility of peptides of the invention, it is possible to add reporter group(s) to the peptide backbone. For example, poly-histidine can be added to a peptide to purify the peptide on immobilized metal ion affinity chromatography (Hochuli, E. et al., Bio/Technology, 6:1321-1325 (1988)). In addition, specific endoprotease cleavage sites can be introduced, if desired, between a reporter group and amino acid sequences of a peptide to facilitate isolation of peptides free of irrelevant sequences. In order to successfully desensitize an individual to a protein antigen, it may be necessary to increase the solubility of a peptide by adding functional groups to the peptide or by not including hydrophobic T cell epitopes or regions containing hydrophobic epitopes in the peptides.

To potentially aid proper antigen processing of T cell epitopes within a peptide, canonical protease sensitive sites can be recombinantly or synthetically engineered between regions, each comprising at least one T cell epitope. For example, charged amino acid pairs, such as KK or RR, can be introduced between regions within a peptide during recombinant construction of the peptide. The resulting peptide can be rendered sensitive to cathepsin and/or other trypsin-like

enzymes cleavage to generate portions of the peptide containing one or more T cell epitopes. In addition, such charged amino acid residues can result in an increase in solubility of a peptide.

Site-directed mutagenesis of DNA encoding a peptide of the invention can be used to modify the structure of the peptide. Such methods may involve PCR (Ho et al., Gene, 77:51-59 (1989)) or total synthesis of mutated genes (Hostomsky, Z., et al., Biochem. Biophys. Res. Comm., 161:1056-1063 (1989)). To enhance bacterial expression, the aforementioned methods can be used in conjunction with other procedures to change the eucaryotic codons in DNA constructs encoding peptides of the invention to ones preferentially used in E. coli.

Specific examples of peptides of the invention modified in accordance with one or more of the modification procedures discussed above include but are not limited to modifications to peptide DPI-23.1 as shown in Fig. 28 and to peptide DPII-22 as shown in Fig. 28. More specifically, modifications to peptides 23.1 include the addition of charged amino acids (23.1.2) charged amino acid pairs (23.1.1) to increase solubility and replacement of a cysteine residue with serine 23.1.3 or glutamic acid (23.1.4) to increase solubility. Changes to peptide 22 include the addition of charged amino acid pairs (22.1 and 22.2) to increase solubility.

The present invention also provides nucleic acids having sequences encoding peptides of the invention. Nucleic acid sequences used in any embodiment of this invention can be cDNA as described herein, or alternatively, can be any oligodeoxynucleotide sequence having all or a portion of a sequence represented herein, or their functional equivalents. Such oligodeoxynucleotide sequences can be produced chemically or mechanically, using known techniques. A functional equivalent of an oligonucleotide sequence is one which is 1) a sequence capable of hybridizing to a complementary oligonucleotide to which the sequence (or corresponding sequence portions) of SEQ ID NO:1, SEQ ID NO: 3, SEQ ID NO: 5 and SEQ ID NO: 7, or fragments thereof hybridizes, or 2) the sequence (or corresponding sequence portion) complementary to SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5 and SEQ ID NO: 7 and/or 3 a sequence which encodes a product (e.g., a polypeptide or peptide) having the same functional characteristics of the product encoded by the sequence (or corresponding sequence portion) of SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5 and SEQ ID NO: 7. Whether a functional equivalent must meet one or more criteria will depend on its use (e.g., if it is to be used only as an oligoprobe, it need meet only the first or second criteria and if it is to be used to produce a peptide of the present invention, it need only meet the third



criterion).

This invention is further illustrated by the following non-limiting examples.

#### Example I Native Mite Allergen Purification

What follows is a description of the work done to purify the group I and group II allergens of the house dust mites Dermatophagoides pteronyssinus and Dermatophagoides farinae in their native form as primary antigens for human T-cell epitope mapping.

All four protein allergens, Der f I, Der p I, Der f II, and Der p II, were immunoaffinity purified from spent mite culture media obtained from either Commonwealth Sera Laboratories Melbourne, Australia or Dr. Larry G. Arlian at Wright State University Dayton, Ohio. A 10% (wt./vol.) aqueous extract of dessicated spent mite culture media was prepared in PBS (Phosphate Buffered Saline) with stirring overnight at 4°C. Insoluble material was removed by centrifugation at 10,000 X g for 1 hour at 4°C. The supernatant was then filtered on a vacuum manifold through Whatman #1 paper, and re-centrifuged at 15,000 X g for 1 hour at 4°C. A final filtration was carried out through a 0.45 m cellulose acetate filter.

Monoclonal antibodies 4C1 and 6D6 (University of Virginia, NC) were used for immunoaffinity purification of group I or group II mite allergens respectively (Chapman et al., J. Allergy Clin. Immunol. 80: 1479-1484 (1987); Heymann et al., J. Allergy Clin. Immunol. 83: 1055-1067 (1989)). The 4C1 monoclonal antibody reacts with an epitope shared by both the Der f I and Der p I proteins; similarly, the 6D6 monoclonal antibody reacts with both the Der f II and Der p II proteins.

For each monoclonal antibody, ascites fluid was cut in 50% ammonium sulfate and the antibodies coupled to CNBr-activated Sepharose 4B (Pharmacia) in 100 mM NaHCO<sub>3</sub>, 500 mM NaCl, pH 8.3, overnight at 4°C.

Monoclonal antibody columns were equilibrated in PBS and the filtered extracts loaded at 15 ml per hour. The column was then washed in 20 volumes of PBS, after which a more stringent wash of 20 column volumes was carried out with PBS supplemented with 500 mM NaCl. Proteins were eluted in 500 mM NaCl, 100 mM glycine pH 11.0, and fractions evaluated for protein content by spectrophotometric absorbance at 280 nm. Peak fractions were pooled and dialyzed extensively against PBS, concentrated with a negative pressure dialysis device (obtained from Amicon, Beverly MA) and were used in T-cell epitope mapping studies of the mite group I and group II allergens. Recovered proteins

were obtained at purities ranging from 80% (group II) to 90% (group I).

Reverse Phase HPLC chromatography was applied to further purify the immunoaffinity purified group II mite protein allergen according to the conditions in Heymann et al., J. Allergy Clin. Immunol. 83: 1055-1067 (1989). Briefly, immunoaffinity purified protein was applied to a 5  $\mu$ m 300 Å C-8 column (Applied Biosystems Inc.) in 0.1% vol/vol. TFA/H<sub>2</sub>O. The flow rate for the column was 1 ml/min. with a gradient of 0-60% acetonitrile/0.1% TFA over 60 minutes. Group II proteins eluted around 45% acetonitrile/0.1% TFA. Fractions were analyzed for purity by SDS-polyacrylamide gel electrophoresis followed by densitometric scanning. Those fractions with group II protein of purity greater than 90% were subsequently utilized for human T-cell mapping of the allergen.

### Example II Recombinant Mite Allergen Expression

What follows is a description of the work done to produce the group I and group II allergens of the house dust mites Dermatophagoides pteronyssinus and Dermatophagoides farinae as recombinant proteins in E. coli.

All four protein allergens, Der f I, Der p I, Der f II, and Der p II, were fused at their mature amino termini with the leader sequence MGHHHHHHEF (where amino acids EF are encoded by the EcoR I restriction site GAATTC). Since the H<sub>6</sub> stretch of amino acids coordinates Ni<sup>++</sup> ions on NTA agarose columns (Diagen GmbH), this activity was exploited in the purification of the recombinant proteins (Hochuli et al., Biotechnology 86: 1321-1325 (1988)). Ultimately, all four allergens were subcloned into the expression vector pET 11d (Studier et al., Methods In Enzymology 185: 60-88 (1990)) under the transcriptional control of the phage T7 gn 10 promoter.

The cDNAs encoding the group I allergens from D. pteronyssinus and D. farinae were obtained from Dr. Wayne Thomas in plasmid form as subclones from  $\lambda$ gt11 (Chua et al., J. Exp. Med. 167: 175-182 (1988); Dilworth et al., Clin. Exp. Allergy 21: 25-32 (1991)). The Der p I cDNA had been subcloned from an M13 RF plasmid as an EcoRI fragment into pUC18 by Dr. Roland Buelow at ImmuLogic (Palo Alto), while the Der f I cDNA was manipulated directly from the M13mp19 RF plasmid Df I(1).

Initially the cDNAs were subcloned into the expression vector pTrc99A His<sub>6</sub> Insert RRRS which is a modified version of pTrc99A (Amann et al., Gene 69: 301-315 (1988)). The original vector was modified by the addition of a synthetic adaptor (consisting of two complimentary oligonucleotides) encoding the leader sequence MGHHHHHHEF between its NcoI (MG) and EcoRI (EF) sites at

the 5' end of the polylinker, and an RRS (Retro Regulatory Sequence) into its Hind III site at the polylinker's 3' end. The leader sequence was used as a purification aid as described above, while the RRS was added to enhance recombinant message stability and thereby increase recombinant protein yield (Skoglund et al., Gene 88: 1-5 (1990)). Lastly, an insert, in this case an Amb a I.1 cDNA encoding the major allergen of the short ragweed (Rafnar et al., J. Biol. Chem. 226: 1229-1236 (1991)) was subcloned in frame with the H<sub>6</sub> leader as an EcoRI to PstI fragment.

To express the mite group I allergens, the Amb a I.1 cDNA was excised by EcoRI/Hind III digestion and replaced by adaptors with  $\phi$ EcoRI/Hind III overhangs (composed of a pair of complimentary oligonucleotides). These adaptors (Fig. 2a) encoded the first 5 amino acids, up to the Pst I site, of the mature Der p I NH<sub>2</sub> terminus, and the first 10 amino acids, up to the HpaI site, of the mature Der f I NH<sub>2</sub> terminus. Upon ligation of the EcoRI site of the vector and the  $\phi$ EcoRI site in the adaptors, the EcoRI site in the vector was destroyed, leaving the EcoRI site encoded internal to the adaptor as the sole EcoRI site in the intermediate constructs pTrc99A His<sub>6</sub> 5' pl RRS and pTrc99A His<sub>6</sub> 5' fl RRS. The Der p I cDNA was inserted as a PstI/EcoRI fragment into PstI/EcoRI digested pTrc99A His<sub>6</sub> 5' pl RRS, while the Der f I cDNA was inserted as a HpaI/EcoRI fragment into HpaI/EcoRI digested pTrc99A His<sub>6</sub> 5' fl RRS. The sequence of the 5' end of each construct, pTrc99A His<sub>6</sub> 5' pl RRS and pTrc99A His<sub>6</sub> fl RRS, was verified by dideoxy chain termination DNA sequencing using a Sequenase™ II kit (U.S. Biochemicals). Both the H<sub>6</sub> pl and H<sub>6</sub> fl coding cassettes were excised by NcoI/NheI digestion (an NheI site existed at the 3' end of the RRS adaptor) and inserted into NcoI/NheI digested pET11d. These two constructs, pET11d His<sub>6</sub> pl RRS and pET11d His<sub>6</sub> fl RRS, were transformed into competent BL21 [DE3] bacteria for expression of the recombinant proteins. BL21 [DE3] contains a recombinant phage  $\lambda$  lysogen, DE 3, with a phage T7 RNA polymerase gene under the transcriptional control of the lac UV5 promoter. T7 RNA polymerase gene expression is induced by the addition of IPTG (Isopropyl-B-D-thiogalactopyranoside), which in turn leads to high level expression of the recombinant gene subcloned 3' of the pET vector's T7 gn 10 promoter.

The cDNAs encoding the group II allergens from D. pteronyssinus and D. farinae were also obtained from Dr. Wayne Thomas in plasmid form as subclones from  $\lambda$ gt11 (Chua et al., Int Arch. Appl. Immun. 91: 118-123 (1990); Trudinger et al., Clin. Exp. Allergy 21: 33-37 (1991)). The original Der p II

cDNA was subcloned from an M13RF plasmid into the pCA and pGEX vectors by Dr. Roland Buelow at ImmuLogic (Palo Alto). Dr. Thomas' group had supplied the Der f II cDNA as a subclone in pGEX. Both pGEX plasmids harboring group II cDNAs were used as templates for PCR amplification with the same 5' sense/3' antisense primer pair (Fig. 2b). The primers were designed to fuse an EcoRI site (GAATTC encoding the amino acids EF) in frame with the NH<sub>2</sub> terminus of the mature group II proteins and place a PstI site 3' of the group II coding region. An MJ Research Thermal Controller with a program of 30 X (94°C 1 min./55°C 1 min. 30 sec./72°C 2 min.) was used in conjunction with reagents from a Perkin Elmer - Cetus Gene Amp kit for PCR amplification. The PCR products were EcoRI/PstI digested and subcloned into EcoRI/PstI digested M13mp19RF. DNA sequence analysis was performed to verify the sequence of the PCR products. Correct M13RF were EcoRI/PstI digested, their group II cDNA inserts isolated, and subcloned into EcoRI/PstI digested pTrc99A His<sub>6</sub> Amb a I.1 RRS (which served to exchange the group II cDNAs with the ragweed cDNA (Fig. 1)).

The Der f II cDNA possessed a sequence polymorphism at position 54 (i.e., threonine residue in place of isoleucine). To alter this polymorphism, site directed mutagenesis of the T<sub>54</sub> residue in the Der f II cDNA was performed using a Muta-Gene kit from Bio-Rad Laboratories, based on the method of Kunkel, Proc. Natl. Acad. Sci. USA 82: 488-492 (1985). The original M13mp19RF with the T<sub>54</sub> Der f II cDNA was transformed into CJ236 bacteria, which tolerate the incorporation of uracil in place of thymidine during DNA replication, and single stranded phage DNA prepared as template. A mutagenic 17 base pair primer (Fig. 2b) was annealed to the phage template DNA. T4 DNA polymerase was used to copy the template DNA primed by the mutagenic oligonucleotide, and T4 DNA ligase served to seal gaps in the DNA strand. The reaction was transformed into MV1190 bacteria, which are wild type for the editing of uracil residues from DNA and therefore selectively replicate the mutagenized (non-uracil containing) strand, and single stranded phage DNA prepared from recombinant (white) plaques. Several recombinants were subjected to DNA sequence analysis and Der f II cDNAs with the corrected I<sub>54</sub> sequence subcloned as EcoRI/PstI fragments into EcoRI/PstI digested pTrc99A His<sub>6</sub> Amb a I.1 RRS.

Since one previous work had shown that the pET11d vector was, in most cases, capable of expressing recombinant proteins at higher levels than the pTrc99A vector, the two mite group II cDNAs were subcloned as H<sub>6</sub> fusion

proteins into T7 vector. pTrc ppA His<sub>6</sub> f II RRS and pTrc99A His<sub>6</sub> p II RRS were Nco I/NheI digested, the cDNA inserts isolated, and subcloned into NcoI/NheI digested pET11d His<sub>6</sub> pl (Fig. 1). Recombinant plasmids were transformed into BL 21 [DE3] bacteria for expression.

BL21 DE3 host bacteria harboring the pET11d mite allergen expression constructs were freshly streaked onto a BHI agar plate (3.7% wt./vol. Difco Brain Heart Infusion; 1.5% wt./vol. Difco agar) supplemented with 200 µg/ml ampicillin and incubated overnight at 37°C. A single colony was inoculated into a 2 ml of 200 µg/ml ampicillin/BHI media (3.7% wt./vol. Difco Brain Heart Infusion) and shaken at 300 rpm at 37°C until turbid but not saturated. The 2 ml culture was then added to 100 ml of 200 µg/ml ampicillin/BHI media, shaken at 300 rpm at 37°C until turbid but not saturated, at which point the culture was divided into 18 X 500 ml (9 litres) of 200 µg/ml ampicillin/BHI media and shaken at 300 rpm at 37°C. When the OD<sub>595</sub> of the culture reached 1.0, expression of the recombinant molecules was induced by the addition of IPTG to 400 µM, and allowed to continue for two hours.

Bacteria were harvested by centrifugation at 10,000 X g for 15 minutes, and resuspended in 1/20<sup>th</sup> volume of lysis buffer (0.2 mg/ml lysozyme, 100 mM NaPO<sub>4</sub> pH 8.0, 50 mM NaCl), incubated on ice for 30 minutes, and frozen at -70°C. The frozen bacteria were fractured by a quick thaw at 37°C and then sonicated 5 times for 20 seconds at 30 second intervals. The sonicated samples were centrifuged at 15,000 X g to separate soluble and particulate bacterial proteins. The soluble proteins were poured off, and the pelleted protein resuspended in 6 M guanidine HCl, 100 mM 2-mercaptoethanol, 100 mM NaPO<sub>4</sub>, 10 mM Tris pH 8.0. This suspension was subjected to centrifugation at 15,000 X g, and the supernatant removed, adjusted to pH 8.0 with 10 N NaOH, and applied to an NTA agarose column that had been equilibrated in 6 M guanidine HCl, 100 mM NaPO<sub>4</sub>, 10 mM Tris pH 8.0. The column was washed in 6 M guanidine HCl, 100 mM NaPO<sub>4</sub>, 10 mM Tris pH 8.0 until the OD<sub>280</sub> of the effluent reached background. The column buffer was then switched to 8 M urea, 100 mM NaPO<sub>4</sub>, 10 mM Tris pH 8.0. After equilibration, a more stringent wash was performed in 8 M urea, 100 mM NaOAc, 10 mM Tris pH 6.3 until the OD<sub>280</sub> of the effluent reached background. Recombinant mite protein (as an H<sub>6</sub> fusion) was then eluted in 8 M urea, 100 mM NaOAc, 10 mM Tris pH 4.5 and collected in aliquots whose OD<sub>280</sub> profile was monitored. The protein peak was dialyzed 3 times into 500 volumes of PBS for human T-cell analysis. Yield ranged from 10 to 70 mg of

recombinant protein per liter with purity (as determined by densitometric scanning) ranging from 80 (Der f II) to 95%.

To further purify the recombinant Der f II protein allergen, Reverse Phase HPLC chromatography was applied. Approximately 100 mg of His<sub>6</sub>-Der f II protein was reduced in 20 mM DTT at 36°C for 30 minutes and then applied to a Pharmacia PRO RPC HR 10/10 column in 0.1% vol./vol. TFA/H<sub>2</sub>O. The flow rate for the column was 1.5 ml/min. with a gradient of 0-70% acetonitrile in 0.1% TFA over 40 minutes, followed by a gradient of 70-100% acetonitrile in 0.1% TFA. His<sub>6</sub>-Der f II protein eluted between 54-96% acetonitrile. Fractions detected at 214 nm and 280 nm were analyzed for purity by SDS-polyacrylamide gel electrophoresis/densitometric scanning. Those fractions with His<sub>6</sub>-Der f II protein of purity greater than 95% were subsequently utilized for human T-cell mapping of the allergen. Yield from the preparative Reverse Phase HPLC was approximately 69%.

#### Determination of Nucleotide Sequence Polymorphisms in the Der p I, Der p II and Der f II Allergens

It was expected that there were sequence polymorphisms in the nucleic acid sequence coding for Der p I, Der p II, Der f I and Der f II, due to natural allelic variation among individual mites. Several nucleotide and resulting amino acid sequence polymorphisms have been discovered during the sequencing of different Der p I, Der p II and Der f II clones. The amino acid sequence polymorphisms are shown in Figs. 22, 23 and 24.

#### Example III Synthesis of Overlapping Peptides

Der p I, Der f I, Der p II, and Der f II overlapping peptides as shown in Figs. 3 and 4 were synthesized using standard Fmoc/tBoc synthetic chemistry and purified by dialysis or Reverse Phase HPLC. The amino acid residues of the synthesized peptides are in brackets by the peptide name and the amino acid sequence (in single letter code) is next to the peptide name. The peptide names are consistent throughout the Figures. The Der p I, Der f I, Der p II and Der f II proteins were divided into overlapping peptides in such a way that the overlapping peptides of Der p I and Der f I as well as for Der p II and Der f II have corresponding amino acid residue numbers, e.g. DP I-1 and DF I-1 both contain amino acid residues 1-20 of the Der p I and Der f I allergens, respectively. This correspondence in amino acid position between the Der p and Der f peptides was done purposefully in order to best test for cross-

reactivity of Der p and Der f T cell epitopes and, thus, determine peptides which, upon administration to an individual sensitive to dust mite, would treat sensitivity to both Der p and Der f allergens. In the design of the overlapping peptides the relationship of the Group I and Group II allergens at the level of T cell cross-reactivity was considered. In addition, the function of the Group I allergens as serine proteases was considered and the amino acid sequences of other known serine proteases, e.g., papain, actinidin, were examined to identify similar conserved and variable regions within the Group I allergens. It was expected that conserved regions within the Group I allergens would contain "shared" T cell epitopes.

#### **Example IV Mite Allergic Patient Primary T Cell Responses to Der p I and Der p II Proteins and Peptides**

Peripheral blood mononuclear cells (PBMC) were purified by Ficoll-Hypaque centrifugation of a peripheral blood specimen from mite-allergic patient R.B. and were assayed for proliferation in response to various antigens, i.e., affinity-purified Der p I, affinity purified Der p II, various Der p I and Der p II peptides. For assay,  $5 \times 10^4$  PBMC were cultured in triplicate microwells for 7 days at 37°C in the presence of various concentrations of antigen in 200  $\mu$ l RPMI-1640 containing 5% human AB serum. Each well then received 1  $\mu$ Ci tritiated thymidine for 16 hours. The counts incorporated were collected onto glass fiber filters and processed for liquid scintillation counting. Table I shows the results of this assay. The CPM +/- standard deviation are shown. The stimulation index of each response (S.I.) is the ratio of the  $^3$ H-thymidine CPM incorporated by the cells in response to antigen divided by the  $^3$ H-thymidine CPM incorporated by cells in medium only. The results indicate that this patient responds with an S.I. of at least 2.0 to peptides DP I-1, DP I-3, DP I-8, DP I-10, DP I-5.2, DP II-4 and DP II-9. Thus, these peptides contain Der p I or Der p II T cell epitopes recognized by T cells from this particular allergic patient.

TABLE I

<u>Antigen</u>	<u>Concentration</u> <u>µg/ml</u>	<u>CPM ± S.D.</u>	<u>S.I.</u>
Medium	--	1071± 30	--
Der p I	10	920±15	0.9
	30	2122±93	2.0
	100	1492±13	1.4
DP I-1	10	1099±48	1.0
	30	3527±73	3.3
	100	2746±81	2.6
DP I-2	10	1395±47	1.3
	30	1283±34	1.5
	100	1486±38	1.4
DP I-3	10	2608±52	2.4
	30	1561±13	1.5
	100	5252±67	4.9
DP I-8	10	1439±32	1.3
	30	1045±32	1.0
	100	2272±40	2.1
DP I-10	10	1936±50	1.8
	30	3042±89	2.8
	100	2644±63	2.5
DP I-5.2	10	1374±20	1.3
	30	2241±87	2.1
	100	3132±111	2.9
Der p II	10	1113±35	1.0
	30	2104±43	2.0
	100	1057±27	1.0
DP II-4	10	2126±25	2.0
	30	1979±94	1.8
	100	2314±116	2.2
DP II-9	10	3970±87	3.7
	30	4464±86	4.2
	100	2237±53	2.1



**Example V T Cell Epitope Studies with Der p I**

Peripheral blood mononuclear cells (PBMC) were purified by Ficoll-Hypaque centrifugation of 60 ml of heparinized peripheral blood from house dust mite-allergic individuals who exhibited clinical symptoms of mite allergy and who were skin test positive for house dust mite.

$10^7$  PBMC from individual 543 were cultured in 10 ml RPMI-1640 containing 5% pooled human AB serum and supplemented with glutamine, penicillin, streptomycin and HEPES buffer in the presence of 20  $\mu\text{g/ml}$  purified native Der p I/ml at 37°C for 7 days. Viable cells were then purified by Ficoll-Hypaque centrifugation and cultured for 2 additional weeks in RPMI-1640/5% AB serum containing 5 units recombinant human IL-2/ml and 5 units recombinant human IL-4/ml. The resting T cells were then tested in a secondary proliferation assay to assess T cell responses to various house dust mite proteins and peptides. For assay,  $2 \times 10^4$  resting T cells were cultured in 200  $\mu\text{l}$  of RPMI-1640/5% AB serum for 3 days at 37°C in the presence of  $2 \times 10^4$  autologous Epstein-Barr virus transformed B cells (20,000 Rads) as antigen presenting cells with various concentrations of purified native Der p I or synthetic Der p I peptides. Each well then received 1  $\mu\text{Ci}$  tritiated thymidine for 16 hours. The counts incorporated were collected onto glass fiber filters and processed for liquid scintillation counting. Medium alone, acting as negative control, contained no allergen or peptide. The results of this experiment indicate that this particular patient responds with an S.I. of at least 2.0 to several peptides derived from the Der p I protein, including DP I-1, DP I-2, DP I-4, DP I-11, DP I-5, DP I-13, DP I-15, DP I-6.1, DP I-8, DP I-9, DP I-16, DP I-10 and DP I-17 (data not shown).

The above procedure was followed with a number of other house dust mite allergic individuals except a) in individual cases, the length of time of cultivation with IL-2 and IL-4 varied; b) in individual cases, the T cells were primed with either purified native (N) or recombinant (R) Der p I protein at either 20  $\mu\text{g/ml}$  or 10  $\mu\text{g/ml}$ ; and c) in individual cases, x-irradiated (3500 Rads) autologous PBMC were used as antigen presenting cells in the secondary proliferation assay. In addition, three peptides (DP I-11 (SEQ ID NO: 117), DP I-12 (SEQ ID NO: 118), and DP II-3 (SEQ ID NO: 119)) were found to contain a low number of conservative changes from the native sequence in their amino acid sequence. Three additional peptides (DP I-11.1 (SEQ ID NO: 13), DP I-12.1 (SEQ ID NO: 14) and DP II-3.1 (SEQ ID NO: 43)) were synthesized with no changes from the native sequence. Some T cell

analysis was done with the original peptides (i.e., DP I-11, DP I-12 and DP II-3). Following T cell analysis conducted with the additional peptides (i.e., DP I-11.1, DP I-12.1 and DP II-3.1) no significant difference in mean S.I. or percentage of positive responses between the original peptides and the additional peptides was detected. Thus, the data from both groups of peptides was pooled.

Individual results were considered positive and used if the individual responded to the Der p I protein and at least one peptide derived from Der p I at an S.I. of 2.0 or greater. A summary of the results of 33 positive experiments is shown in Fig. 5. The resting T cell lines primed with recombinant or native Der p I-stimulated PBMC were tested for reactivity to synthetic Der p I peptides. The maximum response for each peptide in a titration of the antigen is expressed as the T cell stimulation index (S.I.). The S.I. is the counts-per-minute (CPM) incorporated by cells in response to the peptide divided by the CPM incorporated by cells in medium only. An S.I. value greater than the background level indicates that the peptide contains a T cell epitope. However, only individual S.I. values greater than or equal to 2.0 (a response two-fold or greater over background), referred to herein as "positive" results, were used in calculating mean T cell stimulation indices for each peptide for the patient or group of patients tested. In parentheses above each bar on the histogram are the mean T cell stimulation indices calculated after discarding the highest and lowest positive responses for each peptide to minimize the effect of extreme outliers. The T cell stimulation index is calculated by:

$$\frac{(\text{CPM of T cell} + \text{APC} + \text{Antigen})}{\text{CPM of T cell} + \text{APC} + \text{Control}}$$

The bar represents the cumulative rank of the peptide response in the group of patients. To determine the cumulative rank, the 5 peptides with the highest S.I. in each individual were determined and assigned a numerical rank in descending order, with 5 representing the strongest response. The ranks for each peptide were then summed in the group of patients to determine the cumulative rank for the peptide. Above each bar is the percent of positive responses with an S.I. of at least 2 to the peptide in the group of patients tested. Given the percent positive and the mean T cell stimulation index, the positivity index (P.I.) for each peptide can be calculated. The P.I.

for each individual is determined by multiplying the mean S.I. by the percent of individuals, in a population of individuals sensitive to house dust mite (e.g. preferably at least 15 individuals, more preferably at least 30 individuals or more) who responded with an S.I. of at least 2.0 to that peptide (e.g., for DP I-1 in Fig. 5, the P.I. would be about 343 (73% x 4.7). The P.I. therefore represents both the strength of a T cell response to a peptide (S.I.) and the frequency of a T cell response to a peptide in a population of individuals sensitive to house dust mite. Fig. 5 demonstrates that peptides DP I-1, DP I-2, DP I-3, DP I-4, DP I-5, DP I-6.1, DP I-7.1, DP I-8, DP I-9, DP I-16, and DP I-10 contain significant regions of T cell reactivity in this panel of patients.

#### Example VI T Cell Epitope Studies with Der f I

Experiments similar to those of Example V were performed to determine the T cell-reactive areas of the Der f I protein. For example, PBMC from house dust mite-allergic patient 783 were isolated as described in Example V and were stimulated in vitro with recombinant purified Der f I at 20 µg/ml. The results of the proliferation assay with Der f I peptides using x-irradiated (3500 Rads) autologous PBMC as antigen presenting cells indicate that T cells from this patient respond to the peptides DF I-8.1, DF I-9, DF I-6, DF I-10, DF I-2.1, DF I-3, DF I-11, DF I-5, DF I-1, and DF I-17 (data not shown).

The above procedure was followed in a number of patients except in individual cases, T cell lines were primed with affinity purified Der f I at 20 µg/ml or at 10 µg/ml and x-irradiated (25,000 Rads) autologous Epstein-Barr virus transformed B cells were used as antigen presenting cells. A summary of the results of 16 positive experiments is shown in Fig. 6. The data was analyzed as described in Example V. The data indicate that significant areas of T cell reactivity in the Der f I protein are found in the peptides DF I-1, DF I-2, DF I-3, DF I-4, DF I-11, DF I-5, DF I-6, DF I-7, DF I-14, DF I-15, DF I-8.1 and DF I-9.

### Example VII A Study Indicating the Cross-reactivity of Der p I and Der f I T Cell Epitopes

The Der p I and Der f I proteins are very homologous (81% identity). Thus, experiments, similar to those of Example V, were carried out to determine the T cell responses of Der p I primed T cell lines when challenged with various Der p I peptides and substantially matching Der f I peptides. T cell lines were primed *in vitro* as described in Example V and tested for response to a set of substantially matching Der p I and Der f I peptides (e.g., DP I-1 (amino acid residues 1-20 of Der p I) or DF I-1 (amino acid residues 1-20 of Der f I). The data was analyzed as described in Example V except the highest and lowest S.I. values of the positive responses to each peptide were not omitted from the mean S.I. calculations. A summary of a number of such experiments is shown in Fig. 7. The results of 14 positive experiments indicate that Der p I-primed T cells respond to various Der f I peptides indicating cross-reactivity within the Group I allergens. Der p I primed T cells respond significantly to peptides DF I-1, DF I-2, DF I-3, DF I-4, DF I-11, DF I-12, DF I-15, DF I-8, DF I-9, DF I-15 and DF I-6. In some patients, the Der f I peptide was a more potent stimulator of Der p I-primed T cells than the corresponding Der p I peptide. Fig. 8 shows the results of inverse experiments in which T cells from a number of patients were primed *in vitro* to the Der f I protein and analyzed for response to various Der p I peptides and a set of substantially matching Der f I peptides. The results of 8 positive experiments indicate that Der f I primed T cells respond significantly to peptides DP I-1, DP I-3, DP I-4, DP I-11/11.1, DP I-14, DP I-5, DP I-15, and DP I-8.

### Example VIII T Cell Epitope Studies with Der p II.

Experiments similar to those of Example V were performed to determine the T cell-reactive areas of the Der p II protein. For example, PBMC from house dust mite-allergic patient 348 were isolated as described in Example V and were stimulated *in vitro* with 20 µg/ml purified native Der p II. The results of a proliferation assay using x-irradiated (25,000 Rads) Epstein-Barr virus transformed autologous B cells as antigen-presenting cells with various Der p II peptides demonstrate that this particular patient responds well to peptides DP II-1, DP II-7, DP II-8, DP II-2, and DP II-9 (data not shown).

The above procedure was followed with a number of patients except in individual cases, T cell lines were primed with recombinant Der p II at 20 µg/ml or at 3 µg/ml and x-irradiated (3500 Rads) autologous PBMC were used as antigen-presenting cells. A summary of the results of 26 positive experiments is shown in Fig. 9. The data was analyzed as described in Example V, except the ranked sum of peptide responses was analyzed assigning a value of 3, 2 or 1 to the three highest S. I. responses. Areas of significant T cell reactivity within the Der p II protein for this panel of patients are found in peptides DP II-1, DP II-2, DP II-3, DP II-4, DP II-7, DP II-8 and DP II-9.

#### Example IX T Cell Epitope Studies with Der f II

Experiments similar to those of Example V were performed to determine the T cell-reactive areas of the Der f II protein. For example, PBMC from house dust mite-allergic patient 384 were stimulated *in vitro* with purified recombinant Der f II and the T cell line was then challenged in the presence of x-irradiated (25,000 Rads) autologous Epstein-Barr virus transformed B cells as antigen presenting cells with various overlapping Der f II peptides. The results of this proliferation assay indicate that T cells from this particular patient respond well to peptides DF II-1, DF II-2, DF II-3.1, DF II-4.5, DF II-15, DF II-16, and DF II-19.1 (data not shown).

The above procedure was followed with 10 patients, except in individual cases, T cell lines were primed by stimulating the patient PBMC with 20 µg/ml or 3 µg/ml purified native Der f II, and were assayed in the presence of x-irradiated (3500 Rads) autologous PBMC as antigen-presenting cells. A summary of the results of 10 positive experiments is shown in Fig. 10. The data was analyzed as detailed in Example IX, except the highest and lowest S.I. values of the positive responses to each peptide were not omitted from the calculations. The data indicate that significant areas of T cell reactivity within the Der f II protein are found in peptides DF II-1, DF II-2, DF II-13.1, DF II-4.5, DF II-15, DF II-17, and DF II-19.1.

#### Example X A Study Indicating the Cross-Reactivity of Der p II and Der f II T Cell Epitopes

A study similar to that described in Example VII was carried out to determine the T cell cross-reactivity of the Der p II and Der f II proteins. T cells primed with the Der f II protein were challenged with various Der f II

peptides and a set of substantially matching Der p II peptides. A summary of the results of 10 positive experiments is shown in Fig. 11. The results indicate that Der f II primed T cells respond significantly to peptides DP II-1, DP II-3/3.1, DP II-4, and DP II-7. Fig. 12 shows the results of inverse experiments in which T cells from a number of patients were primed *in vitro* to the Der p II protein and analyzed for response to various Der f II peptides. The results of 26 positive experiments indicate that Der p II primed T cells respond significantly to peptides DF II-1, DF II-4.5, DF II-15, DF II-17, DF II-18 and DF II-19.1.

#### Example XI Synthesis of Dominant Peptides

Based on the analyses described in Examples V-X, major areas of T cell reactivity within Der p I, Der p II, Der f I and Der f II were identified. In each study, all of the patients tested responded to the protein allergen (e.g., Der p I) and at least one peptide derived from a major area of T cell reactivity within the protein. Seven regions (Region 1, Region 2, Region 3, Region 4, Region 5, Region 6a and Region 6b) of major T cell reactivity were identified in the Der p I and Der f I proteins. These regions are defined as follows: Region 1, amino acid residues 1-28 of the Der p I and Der f I proteins; Region 2, amino acid residues 36-68 of the Der p I and Der f I proteins; Region 3, amino acid residues 74-109 of the Der p I and Der f I proteins; Region 4, amino acid residues 118-139 of the Der p I and Der f I proteins; Region 5, amino acid residues 141-166 of the Der p I and Der f I proteins; and Region 6a, amino acid residues 161-185 of the Der p I and Der f I proteins and Region 6b, amino acid residues 173-201 of the Der p I and Der f I proteins.

Similarly, four regions of major T cell reactivity (Region 7, Region 8, Region 9, and Region 10) were identified in the Der p II and Der f II proteins. These regions are defined as follows: Region 7, amino acid residues 1-26 of the Der p II and Der f II proteins; Region 8, amino acid residues 33-67 of the Der p II and Der f II proteins; Region 9, amino acid residues 79-104 of the Der p II and Der f II proteins; and Region 10, amino acid residues 107-129 of the Der p II and Der f II proteins. Based in part on the T cell reactivity described in Examples V-X, peptides derived from Der p I, Der f I, Der p II, and Der f II were selected and modified by addition or deletion of amino acid residues at either the 5' or 3' end of the peptide. In designing these selected peptides, various factors were considered, including the ranked sum of the overlapping peptides, the percentage of responses with

an S.I. of at least 2.0 to the peptides, the potential cross-reactivity of the peptides, the difficulty of manufacture of the peptides, etc. T cell studies similar to those described in Examples V-X were performed using these selected peptides to more precisely define the major areas of T cell reactivity within Regions 1-6a and 6b of the Der p I and Der f I protein and Regions 7-10 of the Der p II and Der f II protein.

The results of T cell studies using selected peptides derived from the Der p I, the Der f I, the Der p II and the Der f II proteins are shown in Figs. 13-18a-d. The procedure described in Example V was followed with T cell lines from a number of patients primed *in vitro* to the Der p I protein then analyzed for response to selected peptides derived from the Der p I sequence. The results of 33 positive experiments shown in Fig. 13 indicate that the Der p I primed T cells respond significantly to peptides found in peptides DP I-21.1, DP I-21.2, DP I-22.2, DP I-25.2, DP I-22.1, DP I-23.1, DP I-23.2, DP I-26.1, and DP I-28.1.

Similarly, the procedure described in Example VI was followed with T cell lines from 9 patients primed *in vitro* to the Der f I protein then analyzed for response to selected peptides derived from the protein. The data was analyzed as described in Example VI. The results of the 9 patients shown in Fig. 14 demonstrate T cell reactivity to selected peptides from Der f I.

In another experiment, the T cell lines from a number of patients were primed *in vitro* to the Der p I protein and analyzed for response to selected peptides derived from the Der p I protein and a set of substantially matching peptides derived from the Der f I protein. The data from 30 positive experiments was analyzed as described in Example V. As shown in Fig. 15a, the Der p I primed T cells respond significantly to peptides DF I-21.1, DF I-21.2, DF I-23.1, DF I-22.2, DF I-22.3, DF I-22.4, DF I-23.2, DF I-25.1, DF I-26.1 and DF I-27.1. Fig. 15b is a subset of the data shown in Fig. 15a and shows the response of Der p I primed T cells to peptides analyzed by ranked sum. Fig. 15b shows that DPI-23.1 has the highest ranked sum of this group of peptides in this study. Fig. 16a shows the results of the inverse experiment in which T cells from 9 patients were primed *in vitro* to the Der f I protein and challenged with selected Der f I peptides and a set of substantially matching Der p I peptides. The results indicate that Der f I primed T cells from 9 patients respond to selected peptides from Der p I. Fig. 16a shows that DF I-22.1 and DF I-25.1 have the highest stimulation

indexes of this group of peptides. Fig. 16b is a subset of the same data as shown in Fig. 16a and shows the response of preferred Der f I and Der p I peptides is shown. Fig 16b shows that DF1-22.2 has the highest stimulation index of this group of preferred peptides in this experiment.

Another experiment following the procedure described in Example VIII analyzed the response of 29 patients primed *in vitro* to the Der p II protein and challenged with selected peptides derived from the Der p II sequence. Fig. 17a shows that Der p II primed T cells from one patient respond to selected peptides from Der p II. Fig. 17b shows the results from an experiment similar to that shown in Fig. 17a with a set of 30 patients and with the high and low omitted from the mean. Fig. 17b shows that DP11-20.6 has the highest ranked sum of this group of preferred peptides in this study. Fig. 18a shows the inverse experiment in which T cells from 1 patient were primed *in vitro* to the Der f II protein and challenged with selected peptides derived from the Der p II sequence. Fig. 18a shows that Der f II primed T cells from 10 patients respond to selected peptides from Der p II. As shown in Fig. 18a DP II-25 has the highest stimulation index. Fig. 18b is a subset of the same data shown in Fig. 18a and shows the response of native Der f II primed T cell lines to preferred Der p II peptides analyzed by ranked sum. As is shown in Fig. 18b, DP11-25.2 has the highest ranked sum of the preferred peptides in this study.

#### Example XII Study Indicating Cross-reactivity of Selected Group I and Group II Epitopes

A study similar to that described in Example VII was carried out with T cells from 4 matched patients primed *in vitro* with Group I proteins from Der f and Der p then analyzed for response to selected preferred peptides from Der p I and Der f I. The results in Fig. 18c demonstrate that T cell reactivity to a number of the selected preferred Der p I peptides was essentially equivalent for their Der f I counterpart and vice-versa.

Fig. 18d shows the results of a similar study with T cells from 6 matched patients primed *in vitro* with Group II proteins from Der p and Der f, then analyzed for response to selected preferred Der p II and Der f II peptides. Similar to the results in Fig. 18c, T cell reactivity to a number of the selected preferred peptides of Der p II are essentially equivalent to their Der f II counterparts and vice-versa.



### Example XIII Direct Binding Assay of IgE to Mite Allergen Proteins and Peptides

Corning assay plates (#25882-96) were coated with 5 µg/ml of each coating antigen listed in Figs. 19, 20 and 21 at 50 µl/100ml/well and incubated overnight at 4°C. The coating antigens were removed and the wells are blocked with 0.5% gelatin in PBS, 300 µl/well for 2 hours at room temperature. Pooled human plasma (a mix of plasma samples from 20 patients that were skin test positive for commercial mite extract) was serially diluted with PBS-Tween 20 (PBS with 0.05% nonionic detergent Tween-20 Sigma, St. Louis, MO) and 100 µl/well was added and incubated overnight at 4°C (plasma dilutions were tested in duplicate). The second antibody (biotinylated goat anti-Human IgE, 1:1000, Kirkegaard & Perry Laboratories Inc, Gaithersburg, MD), was added at 100 µl/well for one hour at room temperature. This solution was removed and streptavidin-HRPO, 1:10000, (Southern Biotechnology Associates, Inc., Birmingham, AL) was then added at 100 µl/well for one hour at room temperature (all wells are washed three times with PBS-Tween between each incubation step). TMB Membrane Peroxidase Substrate system (Kirkegaard & Perry Laboratories) was freshly mixed, and added at 100ml/well. The color was allowed to develop for 2-5 minutes. The reaction was stopped by the addition of 100ml/well of 1M phosphoric acid. Plates were read on a Microplate IL310 Autoreader (Biotech Instruments, Winooski, VT) with a 450 nm filter. The absorbance levels of duplicate wells were averaged. The graphed results (log of the dilution versus absorbance) of the ELISA assays are shown in Figs. 19a-b, 20a-b and 21a-h. The order of coating antigens listed vertically in these figure legends corresponds in order from left to right to the coating antigens listed for each histogram.

The results of the ELISA assay shown in Fig. 19b demonstrate good binding of both biochemically purified Der p II and recombinant Der p II (rDer p II) with human IgE and no detectable binding to the Der p II peptides. The IgE binding to the Der p set of peptides and proteins (Figs. 20a and 20b) shows the same pattern of reactivity as the Der f set. That is, no detectable binding to Der f I or Der f II peptides or recombinant Der f I with binding to only biochemically purified Der f I and recombinant and biochemically purified Der f II. In both cases there appears to be better binding to recombinant Der p II or Der f II than to the biochemically purified forms. All the conclusions derived from the above ELISA assay data were

corroborated by another assay method, dot blots on nitrocellulose paper, using the same set of antibody and antigen reagents.

The antigen preparation that was used as a positive control was a mixture of the four major biochemically purified mite allergens (term PMA for Purified Mite Allergen); Der f I, Der f II, Der p I and Der p II. The stock was generated at a concentration of 100 µgs of each protein per millimeter or 400 µgs total protein/ml. This preparation was used on each coated ELISA plate. The results from these ELISA assays are shown in Fig. 21a-h. There is clear binding to either the purified or recombinant protein or the PMA antigen preparation on each plate indicating good IgE reactivity. However, the PMA antigen preparation, does exhibit a high degree of non-specific reactivity shown in the background dilution where no first antibody solution was added. This non-specific reactivity occurs between the PMA antigen and the biotinylated second antibody and does not compromise the finding of specific IgE reactivity to the antigen. Using a quantitative value of two-fold over background at the highest plasma concentration as a positive reading, there is no detectable IgE reactivity to any one of the 56 peptides screened by this assay method.

Although the invention has been described with reference to its preferred embodiments, other embodiments can achieve the same results. Variations and modifications to the present invention will be obvious to those skilled in the art and is intended to cover in the appended claims all such modifications and equivalents that follow in the true spirit and scope of the invention.

## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

- (i) APPLICANT: Kuo, Mei-chang  
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- (ii) TITLE OF INVENTION: T CELL EPITOPES OF THE MAJOR ALLERGENS  
FROM DERMATOPHAGOIDES (HOUSE DUST MITE)
- (iii) NUMBER OF SEQUENCES: 119
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  - (A) ADDRESSEE: LAHIVE & COCKFIELD
  - (B) STREET: 60 STATE STREET SUITE 510
  - (C) CITY: BOSTON
  - (D) STATE: MA
  - (E) COUNTRY: USA
  - (F) ZIP: 02109
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Floppy disk
  - (B) COMPUTER: IBM PC compatible
  - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
  - (D) SOFTWARE: ASCII TEXT
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER: US 07/881,396
  - (B) FILING DATE: 08-MAY-1992
  - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: MANDRAGOURAS, AMY E.
  - (B) REGISTRATION NUMBER: P36,207
  - (C) REFERENCE/DOCKET NUMBER: IMI-012/IPC-017C
- (ix) TELECOMMUNICATION INFORMATION:
  - (A) TELEPHONE: (617) 227-7400
  - (B) TELEFAX: (617) 227-5941

## (2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 834 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
  - (A) NAME/KEY: CDS
  - (B) LOCATION: 1..738

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

AAA AAC CGA TTT TTG ATG AGT GCA GAA GCT TTT GAA CAC CTC AAA ACT  
 48  
 Lys Asn Arg Phe Leu Met Ser Ala Glu Ala Phe Glu His Leu Lys Thr  
 1 5 10 15

CAA TTC GAT TTG AAT GCT GAA ACT AAC GCC TGC AGT ATC AAT GGA AAT  
 96  
 Gln Phe Asp Leu Asn Ala Glu Thr Asn Ala Cys Ser Ile Asn Gly Asn  
 20 25 30

GCT CCA GCT GAA ATC GAT TTG CGA CAA ATG CGA ACT GTC ACT CCC ATT  
 144  
 Ala Pro Ala Glu Ile Asp Leu Arg Gln Met Arg Thr Val Thr Pro Ile  
 35 40 45

CGT ATG CAA GGA GGC TGT GGT TCA TGT TGG GCT TTC TCT GGT GTT GCC  
 192  
 Arg Met Gln Gly Gly Cys Gly Ser Cys Trp Ala Phe Ser Gly Val Ala  
 50 55 60

GCA ACT GAA TCA GCT TAT TTG GCT CAC CGT AAT CAA TCA TTG GAT CTT  
 240  
 Ala Thr Glu Ser Ala Tyr Leu Ala His Arg Asn Gln Ser Leu Asp Leu  
 65 70 75 80

GCT GAA CAA GAA TTA GTC GAT TGT GCT TCC CAA CAC GGT TGT CAT GGT  
 288  
 Ala Glu Gln Glu Leu Val Asp Cys Ala Ser Gln His Gly Cys His Gly  
 85 90 95

GAT ACC ATT CCA CGT GGT ATT GAA TAC ATC CAA CAT AAT GGT GTC GTC  
 336  
 Asp Thr Ile Pro Arg Gly Ile Glu Tyr Ile Gln His Asn Gly Val Val  
 100 105 110

CAA GAA AGC TAC TAT CGA TAC GTT GCA CGA GAA CAA TCA TGC CGA CGA  
 384  
 Gln Glu Ser Tyr Tyr Arg Tyr Val Ala Arg Glu Gln Ser Cys Arg Arg  
 115 120 125

CCA AAT GCA CAA CGT TTC GGT ATC TCA AAC TAT TGC CAA ATT TAC CCA  
 432  
 Pro Asn Ala Gln Arg Phe Gly Ile Ser Asn Tyr Cys Gln Ile Tyr Pro  
 130 135 140

CCA AAT GCA AAC AAA ATT CGT GAA GCT TTG GCT CAA ACC CAC AGC GCT  
 480  
 Pro Asn Ala Asn Lys Ile Arg Glu Ala Leu Ala Gln Thr His Ser Ala  
 145 150 155 160

ATT GCC GTC ATT ATT GGC ATC AAA GAT TTA GAC GCA TTC CGT CAT TAT  
 528  
 Ile Ala Val Ile Ile Gly Ile Lys Asp Leu Asp Ala Phe Arg His Tyr  
 165 170 175

GAT GGC CGA ACA ATC ATT CAA CGC GAT AAT GGT TAC CAA CCA AAC TAT  
 576  
 Asp Gly Arg Thr Ile Ile Gln Arg Asp Asn Gly Tyr Gln Pro Asn Tyr  
 180 185 190

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CAC GCT GTC AAC ATT GTT GGT TAC AGT AAC GCA CAA GGT GTC GAT TAT  
624  
His Ala Val Asn Ile Val Gly Tyr Ser Asn Ala Gln Gly Val Asp Tyr  
195 200 205  
TGG ATC GTA CGA AAC AGT TGG GAT ACC AAT TGG GGT GAT AAT GGT TAC  
672  
Trp Ile Val Arg Asn Ser Trp Asp Thr Asn Trp Gly Asp Asn Gly Tyr  
210 215 220  
GGT TAT TTT GCT GCC AAC ATC GAT TTG ATG ATG ATT GAA GAA TAT CCA  
720  
Gly Tyr Phe Ala Ala Asn Ile Asp Leu Met Met Ile Glu Glu Tyr Pro  
225 230 235 240  
TAT GTT GTC ATT CTC TAAACAAAAA GACAATTTCT TATATGATTG TCACTAATTT  
775  
Tyr Val Val Ile Leu  
245  
ATTTAAATC AAAATTTTTT AGAAAATGAA TAAATTCATT CACAAAAATT AAAAAAAA  
834

## (2) INFORMATION FOR SEQ ID NO:2:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 245 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Lys Asn Arg Phe Leu Met Ser Ala Glu Ala Phe Glu His Leu Lys Thr  
1 5 10 15  
Gln Phe Asp Leu Asn Ala Glu Thr Asn Ala Cys Ser Ile Asn Gly Asn  
20 25 30  
Ala Pro Ala Glu Ile Asp Leu Arg Gln Met Arg Thr Val Thr Pro Ile  
35 40 45  
Arg Met Gln Gly Gly Cys Gly Ser Cys Trp Ala Phe Ser Gly Val Ala  
50 55 60  
Ala Thr Glu Ser Ala Tyr Leu Ala His Arg Asn Gln Ser Leu Asp Leu  
65 70 75 80  
Ala Glu Gln Glu Leu Val Asp Cys Ala Ser Gln His Gly Cys His Gly  
85 90 95  
Asp Thr Ile Pro Arg Gly Ile Glu Tyr Ile Gln His Asn Gly Val Val  
100 105 110  
Gln Glu Ser Tyr Tyr Arg Tyr Val Ala Arg Glu Gln Ser Cys Arg Arg  
115 120 125  
Pro Asn Ala Gln Arg Phe Gly Ile Ser Asn Tyr Cys Gln Ile Tyr Pro  
130 135 140  
Pro Asn Ala Asn Lys Ile Arg Glu Ala Leu Ala Gln Thr His Ser Ala  
145 150 155 160  
Ile Ala Val Ile Ile Gly Ile Lys Asp Leu Asp Ala Phe Arg His Tyr  
165 170 175

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Asp Gly Arg Thr Ile Ile Gln Arg Asp Asn Gly Tyr Gln Pro Asn Tyr
      180                      185                      190
His Ala Val Asn Ile Val Gly Tyr Ser Asn Ala Gln Gly Val Asp Tyr
      195                      200                      205
Trp Ile Val Arg Asn Ser Trp Asp Thr Asn Trp Gly Asp Asn Gly Tyr
      210                      215                      220
Gly Tyr Phe Ala Ala Asn Ile Asp Leu Met Met Ile Glu Glu Tyr Pro
      225                      230                      235                      240
Tyr Val Val Ile Leu
                      245

```

## (2) INFORMATION FOR SEQ ID NO:3:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 588 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 69..509

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

```

CACAAATTCT TCTTTCTTCC TTACTACTGA TCATTAATCT GAAAACAAAA CCAAACAAAC
60
CATTCAAA ATG ATG TAC AAA ATT TTG TGT CTT TCA TTG TTG GTC GCA GCC
110
      Met Met Tyr Lys Ile Leu Cys Leu Ser Leu Leu Val Ala Ala
      1           5           10
GTT GCT CGT GAT CAA GTC GAT GTC AAA GAT TGT GCC AAT CAT GAA ATC
158
Val Ala Arg Asp Gln Val Asp Val Lys Asp Cys Ala Asn His Glu Ile
15           20           25           30
AAA AAA GTT TTG GTA CCA GGA TGC CAT GGT TCA GAA CCA TGT ATC ATT
206
Lys Lys Val Leu Val Pro Gly Cys His Gly Ser Glu Pro Cys Ile Ile
35           40           45
CAT CGT GGT AAA CCA TTC CAA TTG GAA GCC GTT TTC GAA GCC AAC CAA
254
His Arg Gly Lys Pro Phe Gln Leu Glu Ala Val Phe Glu Ala Asn Gln
50           55           60

```

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AAC ACA AAA ACG GCT AAA ATT GAA ATC AAA GCC TCA ATC GAT GGT TTA  
 302  
 Asn Thr Lys Thr Ala Lys Ile Glu Ile Lys Ala Ser Ile Asp Gly Leu  
 65 70 75  
 GAA GTT GAT GTT CCC GGT ATC GAT CCA AAT GCA TGC CAT TAC ATG AAA  
 350  
 Glu Val Asp Val Pro Gly Ile Asp Pro Asn Ala Cys His Tyr Met Lys  
 80 85 90  
 TGC CCA TTG GTT AAA GGA CAA CAA TAT GAT ATT AAA TAT ACA TGG AAT  
 398  
 Cys Pro Leu Val Lys Gly Gln Gln Tyr Asp Ile Lys Tyr Thr Trp Asn  
 95 100 105 110  
 GTT CCG AAA ATT GCA CCA AAA TCT GAA AAT GTT GTC GTC ACT GTT AAA  
 446  
 Val Pro Lys Ile Ala Pro Lys Ser Glu Asn Val Val Val Thr Val Lys  
 115 120 125  
 GTT ATG GGT GAT GAT GGT GTT TTG GCC TGT GCT ATT GCT ACT CAT GCT  
 494  
 Val Met Gly Asp Asp Gly Val Leu Ala Cys Ala Ile Ala Thr His Ala  
 130 135 140  
 AAA ATC CGC GAT TAAATAAACA AAATTTATTG ATTTTGTAAT CACAAATGAT  
 546  
 Lys Ile Arg Asp  
 145

TGATTTTCTT TCCAAAAAAA AAATAAATAA AATTTTGGGA AT  
 588

## (2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 146 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Met Tyr Lys Ile Leu Cys Leu Ser Leu Leu Val Ala Ala Val Ala  
 1 5 10 15  
 Arg Asp Gln Val Asp Val Lys Asp Cys Ala Asn His Glu Ile Lys Lys  
 20 25 30  
 Val Leu Val Pro Gly Cys His Gly Ser Glu Pro Cys Ile Ile His Arg  
 35 40 45  
 Gly Lys Pro Phe Gln Leu Glu Ala Val Phe Glu Ala Asn Gln Asn Thr  
 50 55 60  
 Lys Thr Ala Lys Ile Glu Ile Lys Ala Ser Ile Asp Gly Leu Glu Val  
 65 70 75 80  
 Asp Val Pro Gly Ile Asp Pro Asn Ala Cys His Tyr Met Lys Cys Pro  
 85 90 95  
 Leu Val Lys Gly Gln Gln Tyr Asp Ile Lys Tyr Thr Trp Asn Val Pro  
 100 105 110

Lys Ile Ala Pro Lys Ser Glu Asn Val Val Val Thr Val Lys Val Met  
 115 120 125  
 Gly Asp Asp Gly Val Leu Ala Cys Ala Ile Ala Thr His Ala Lys Ile  
 130 135 140  
 Arg Asp  
 145

## (2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1072 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:  
 (A) NAME/KEY: CDS  
 (B) LOCATION: 36..1001

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CGTTTTCTTC CATCAAAATT AAAAATTCAT CAAAA ATG AAA TTC GTT TTG GCC  
 53 Met Lys Phe Val Leu Ala  
 1 5  
 ATT GCC TCT TTG TTG GTA TTG AGC ACT GTT TAT GCT CGT CCA GCT TCA  
 101  
 Ile Ala Ser Leu Leu Val Leu Ser Thr Val Tyr Ala Arg Pro Ala Ser  
 10 15 20  
 ATC AAA ACT TTT GAA GAA TTC AAA AAA GCC TTC AAC AAA AAC TAT GCC  
 149  
 Ile Lys Thr Phe Glu Glu Phe Lys Lys Ala Phe Asn Lys Asn Tyr Ala  
 25 30 35  
 ACC GTT GAA GAG GAA GAA GTT GCC CGT AAA AAC TTT TTG GAA TCA TTG  
 197  
 Thr Val Glu Glu Glu Glu Val Ala Arg Lys Asn Phe Leu Glu Ser Leu  
 40 45 50  
 AAA TAT GTT GAA GCT AAC AAA GGT GCC ATC AAC CAT TTG TCC GAT TTG  
 245  
 Lys Tyr Val Glu Ala Asn Lys Gly Ala Ile Asn His Leu Ser Asp Leu  
 55 60 65 70  
 TCA TTG GAT GAA TTC AAA AAC CGT TAT TTG ATG AGT GCT GAA GCT TTT  
 293  
 Ser Leu Asp Glu Phe Lys Asn Arg Tyr Leu Met Ser Ala Glu Ala Phe  
 75 80 85  
 GAA CAA CTC AAA ACT CAA TTC GAT TTG AAT GCC GAA ACA AGC GCT TGC  
 341  
 Glu Gln Leu Lys Thr Gln Phe Asp Leu Asn Ala Glu Thr Ser Ala Cys  
 90 95 100  
 CGT ATC AAT TCG GTT AAC GTT CCA TCG GAA TTG GAT TTA CGA TCA CTG  
 389  
 Arg Ile Asn Ser Val Asn Val Pro Ser Glu Leu Asp Leu Arg Ser Leu  
 105 110 115



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CGA ACT GTC ACT CCA ATC CGT ATG CAA GGA GGC TGT GGT TCA TGT TGG  
 437  
 Arg Thr Val Thr Pro Ile Arg Met Gln Gly Gly Cys Gly Ser Cys Trp  
 120 125 130

GCT TTC TCT GGT GTT GCC GCA ACT GAA TCA GCT TAT TTG GCC TAC CGT  
 485  
 Ala Phe Ser Gly Val Ala Ala Thr Glu Ser Ala Tyr Leu Ala Tyr Arg  
 135 140 145 150

AAC ACG TCT TTG GAT CTT TCT GAA CAG GAA CTC GTC GAT TGC GCA TCT  
 533  
 Asn Thr Ser Leu Asp Leu Ser Glu Gln Glu Leu Val Asp Cys Ala Ser  
 155 160 165

CAA CAC GGA TGT CAC GGC GAT ACA ATA CCA AGA GGC ATC GAA TAC ATC  
 581  
 Gln His Gly Cys His Gly Asp Thr Ile Pro Arg Gly Ile Glu Tyr Ile  
 170 175 180

CAA CAA AAT GGT GTC GTT GAA GAA AGA AGC TAT CCA TAC GTT GCA CGA  
 629  
 Gln Gln Asn Gly Val Val Glu Glu Arg Ser Tyr Pro Tyr Val Ala Arg  
 185 190 195

GAA CAA CGA TGC CGA CGA CCA AAT TCG CAA CAT TAC GGT ATC TCA AAC  
 677  
 Glu Gln Arg Cys Arg Arg Pro Asn Ser Gln His Tyr Gly Ile Ser Asn  
 200 205 210

TAC TGC CAA ATT TAT CCA CCA GAT GTG AAA CAA ATC CGT GAA GCT TTG  
 725  
 Tyr Cys Gln Ile Tyr Pro Pro Asp Val Lys Gln Ile Arg Glu Ala Leu  
 215 220 225 230

ACT CAA ACA CAC ACA GCT ATT GCC GTC ATT ATT GGC ATC AAA GAT TTG  
 773  
 Thr Gln Thr His Thr Ala Ile Ala Val Ile Ile Gly Ile Lys Asp Leu  
 235 240 245

AGA GCT TTC CAA CAT TAT GAT GGA CGA ACA ATC ATT CAA CAT GAC AAT  
 821  
 Arg Ala Phe Gln His Tyr Asp Gly Arg Thr Ile Ile Gln His Asp Asn  
 250 255 260

GGT TAT CAA CCA AAC TAT CAT GCC GTC AAC ATT GTC GGT TAC GGA AGT  
 869  
 Gly Tyr Gln Pro Asn Tyr His Ala Val Asn Ile Val Gly Tyr Gly Ser  
 265 270 275

ACA CAA GGC GAC GAT TAT TGG ATC GTA CGA AAC AGT TGG GAT ACT ACC  
 917  
 Thr Gln Gly Asp Asp Tyr Trp Ile Val Arg Asn Ser Trp Asp Thr Thr  
 280 285 290

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TGG GGA GAT AGC GGA TAC GGA TAT TTC CAA GCC GGA AAC AAC CTC ATG  
 965  
 Trp Gly Asp Ser Gly Tyr Gly Tyr Phe Gln Ala Gly Asn Asn Leu Met  
 295 300 305 310  
 ATG ATC GAA CAA TAT CCA TAT GTT GTA ATC ATG TGAACATTTG AAATTGAATA  
 1018  
 Met Ile Glu Gln Tyr Pro Tyr Val Val Ile Met  
 315 320  
 TATTTATTTG TTTTCAAAT AAAACAACACT ACTCTTGCGA GTATTTTTTA CTCG  
 1072

## (2) INFORMATION FOR SEQ ID NO:6:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 321 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Lys Phe Val Leu Ala Ile Ala Ser Leu Leu Val Leu Ser Thr Val  
 1 5 10 15  
 Tyr Ala Arg Pro Ala Ser Ile Lys Thr Phe Glu Glu Phe Lys Lys Ala  
 20 25 30  
 Phe Asn Lys Asn Tyr Ala Thr Val Glu Glu Glu Glu Val Ala Arg Lys  
 35 40 45  
 Asn Phe Leu Glu Ser Leu Lys Tyr Val Glu Ala Asn Lys Gly Ala Ile  
 50 55 60  
 Asn His Leu Ser Asp Leu Ser Leu Asp Glu Phe Lys Asn Arg Tyr Leu  
 65 70 75 80  
 Met Ser Ala Glu Ala Phe Glu Gln Leu Lys Thr Gln Phe Asp Leu Asn  
 85 90 95  
 Ala Glu Thr Ser Ala Cys Arg Ile Asn Ser Val Asn Val Pro Ser Glu  
 100 105 110  
 Leu Asp Leu Arg Ser Leu Arg Thr Val Thr Pro Ile Arg Met Gln Gly  
 115 120 125  
 Gly Cys Gly Ser Cys Trp Ala Phe Ser Gly Val Ala Ala Thr Glu Ser  
 130 135 140  
 Ala Tyr Leu Ala Tyr Arg Asn Thr Ser Leu Asp Leu Ser Glu Gln Glu  
 145 150 155 160  
 Leu Val Asp Cys Ala Ser Gln His Gly Cys His Gly Asp Thr Ile Pro  
 165 170 175  
 Arg Gly Ile Glu Tyr Ile Gln Gln Asn Gly Val Val Glu Glu Arg Ser  
 180 185 190  
 Tyr Pro Tyr Val Ala Arg Glu Gln Arg Cys Arg Arg Pro Asn Ser Gln  
 195 200 205  
 His Tyr Gly Ile Ser Asn Tyr Cys Gln Ile Tyr Pro Pro Asp Val Lys  
 210 215 220

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Gln Ile Arg Glu Ala Leu Thr Gln Thr His Thr Ala Ile Ala Val Ile  
 225 230 235 240

Ile Gly Ile Lys Asp Leu Arg Ala Phe Gln His Tyr Asp Gly Arg Thr  
 245 250 255

Ile Ile Gln His Asp Asn Gly Tyr Gln Pro Asn Tyr His Ala Val Asn  
 260 265 270

Ile Val Gly Tyr Gly Ser Thr Gln Gly Asp Asp Tyr Trp Ile Val Arg  
 275 280 285

Asn Ser Trp Asp Thr Thr Trp Gly Asp Ser Gly Tyr Gly Tyr Phe Gln  
 290 295 300

Ala Gly Asn Asn Leu Met Met Ile Glu Gln Tyr Pro Tyr Val Val Ile  
 305 310 315 320

Met

## (2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 491 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:  
 (A) NAME/KEY: CDS  
 (B) LOCATION: 1..390

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GAT CAA GTC GAT GTT AAA GAT TGT GCC AAC AAT GAA ATC AAA AAA GTA  
 48

Asp Gln Val Asp Val Lys Asp Cys Ala Asn Asn Glu Ile Lys Lys Val  
 1 5 10 15

ATG GTC GAT GGT TGC CAT GGT TCT GAT CCA TGC ATA ATC CAT CGT GGT  
 96

Met Val Asp Gly Cys His Gly Ser Asp Pro Cys Ile Ile His Arg Gly  
 20 25 30

AAA CCA TTC ACT TTG GAA GCC TTA TTC GAT GCC AAC CAA AAC ACT AAA  
 144

Lys Pro Phe Thr Leu Glu Ala Leu Phe Asp Ala Asn Gln Asn Thr Lys  
 35 40 45

ACC GCT AAA ACT GAA ATC AAA GCC AGC CTC GAT GGT CTT GAA ATT GAT  
 192

Thr Ala Lys Thr Glu Ile Lys Ala Ser Leu Asp Gly Leu Glu Ile Asp  
 50 55 60

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GTT CCC GGT ATT GAT ACC AAT GCT TGC CAT TTT ATG AAA TGT CCA TTG  
 240  
 Val Pro Gly Ile Asp Thr Asn Ala Cys His Phe Met Lys Cys Pro Leu  
 65 70 75 80

GTT AAA GGT CAA CAA TAT GAT GCC AAA TAT ACA TGG AAT GTG CCC AAA  
 288  
 Val Lys Gly Gln Gln Tyr Asp Ala Lys Tyr Thr Trp Asn Val Pro Lys  
 85 90 95

ATT GCA CCA AAA TCT GAA AAC GTT GTC GTT ACA GTC AAA CTT GTT GGT  
 336  
 Ile Ala Pro Lys Ser Glu Asn Val Val Val Thr Val Lys Leu Val Gly  
 100 105 110

GAT AAT GGT GTT TTG GCT TGC GCT ATT GCT ACC CAC GCT AAA ATC CGT  
 384  
 Asp Asn Gly Val Leu Ala Cys Ala Ile Ala Thr His Ala Lys Ile Arg  
 115 120 125

GAT TAAAAA AAAA AAATAAATAT GAAAATTTTC ACCAACATCG AACAAAATTC  
 437  
 Asp  
 130

ATAACCAAA ATTTGAATCA AAAACGGAAT TCCAAGCTGA GCGCCGGTTCG CTAC  
 491

## (2) INFORMATION FOR SEQ ID NO:8:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Asp Gln Val Asp Val Lys Asp Cys Ala Asn Asn Glu Ile Lys Lys Val  
 1 5 10 15  
 Met Val Asp Gly Cys His Gly Ser Asp Pro Cys Ile Ile His Arg Gly  
 20 25 30  
 Lys Pro Phe Thr Leu Glu Ala Leu Phe Asp Ala Asn Gln Asn Thr Lys  
 35 40 45  
 Thr Ala Lys Thr Glu Ile Lys Ala Ser Leu Asp Gly Leu Glu Ile Asp  
 50 55 60  
 Val Pro Gly Ile Asp Thr Asn Ala Cys His Phe Met Lys Cys Pro Leu  
 65 70 75 80  
 Val Lys Gly Gln Gln Tyr Asp Ala Lys Tyr Thr Trp Asn Val Pro Lys  
 85 90 95  
 Ile Ala Pro Lys Ser Glu Asn Val Val Val Thr Val Lys Leu Val Gly  
 100 105 110

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Asp Asn Gly Val Leu Ala Cys Ala Ile Ala Thr His Ala Lys Ile Arg  
 115 120 125

Asp

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Thr Asn Ala Cys Ser Ile Asn Gly Asn Ala Pro Ala Glu Ile Asp Leu  
 1 5 10 15  
 Arg Gln Met Arg  
 20

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 27 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Glu Ile Asp Leu Arg Gln Met Arg Thr Val Thr Pro Ile Arg Met Gln  
 1 5 10 15  
 Gly Gly Cys Gly Ser Cys Trp Ala Phe Ser Gly  
 20 25

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 29 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: N-terminal

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Thr Val Thr Pro Ile Arg Met Gln Gly Gly Cys Gly Ser Cys Trp Ala  
1 5 10 15  
Phe Ser Gly Val Ala Ala Thr Glu Ser Ala Tyr Leu Ala  
20 25

## (2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 21 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: N-terminal

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Val Ala Ala Thr Glu Ser Ala Tyr Leu Ala His Arg Asn Gln Ser Leu  
1 5 10 15  
Asp Leu Ala Glu Gln  
20

## (2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 22 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: N-terminal

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

His Arg Asn Gln Ser Leu Asp Leu Ala Glu Gln Glu Leu Val Asp Cys  
1 5 10 15  
Ala Ser Gln His Gly Cys  
20

## (2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 21 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: N-terminal

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Glu Leu Val Asp Cys Ala Ser Gln His Gly Cys His Gly Asp Thr Ile  
1 5 10 15  
Pro Arg Gly Ile Glu  
20

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Gly Asp Thr Ile Pro Arg Gly Ile Glu Tyr Ile Gln His Asn Gly Val  
1 5 10 15  
Val Gln Glu Ser Tyr Tyr Arg Tyr Val Ala Arg Glu  
20 25

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Glu Tyr Ile Gln His Asn Gly Val Val Gln Glu Ser Tyr Tyr Arg Tyr  
1 5 10 15  
Val Ala Arg Glu  
20

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: N-terminal

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

His Asn Gly Val Val Gln Glu Ser Tyr Tyr Arg Tyr Val Ala Arg Glu  
1 5 10 15  
Gln Ser Cys Arg Arg Pro Asn Ala Gln  
20 25

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Gln Ser Cys Arg Arg Pro Asn Ala Gln Arg Phe Gly Ile Ser Asn Tyr  
1 5 10 15  
Cys Gln Ile

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Arg Phe Gly Ile Ser Asn Tyr Cys Gln Ile Tyr Pro Pro Asn Ala Asn  
1 5 10 15  
Lys Ile Arg Glu Ala Leu  
20

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Tyr Pro Pro Asn Ala Asn Lys Ile Arg Glu Ala Leu Ala Gln Thr His  
1 5 10 15  
Ser Ala Ile Ala Val Ile Ile Gly  
20



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## (2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 26 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Ala	Gln	Thr	His	Ser	Ala	Ile	Ala	Val	Ile	Ile	Gly	Ile	Lys	Asp	Leu
1				5				10						15	
Asp	Ala	Phe	Arg	His	Tyr	Asp	Gly	Arg	Thr						
			20					25							

## (2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 26 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Ile	Lys	Asp	Leu	Asp	Ala	Phe	Arg	His	Tyr	Asp	Gly	Thr	Arg	Ile	Ile
1				5					10					15	
Gln	Arg	Asp	Asn	Gly	Tyr	Gln	Pro	Asn	Tyr						
			20					25							

## (2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 23 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Ile	Ile	Gln	Arg	Asp	Asn	Gly	Tyr	Gln	Pro	Asn	Tyr	His	Ala	Val	Asn
1				5					10					15	
Ile	Val	Gly	Tyr	Ser	Asn	Ala									
			20												

## (2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 22 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

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(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

His Ala Val Asn Ile Val Gly Tyr Ser Asn Ala Gln Gly Val Asp Tyr  
1 5 10 15  
Trp Ile Val Arg Asn Ser  
20

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 24 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Gln Gly Val Asp Tyr Trp Ile Val Arg Asn Ser Trp Asp Thr Asn Trp  
1 5 10 15  
Gly Asp Asn Gly Tyr Gly Tyr Phe  
20

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 26 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Gly Asp Asn Gly Tyr Gly Tyr Phe Ala Ala Asn Ile Asp Leu Met Met  
1 5 10 15  
Ile Glu Glu Tyr Pro Tyr Val Val Ile Leu  
20 25

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 28 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: N-terminal

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Thr Asn Ala Cys Ser Ile Asn Gly Asn Ala Pro Ala Glu Ile Asp Leu  
 1 5 10 15

Arg Gln Met Arg Thr Val Thr Pro Ile Arg Met Gln  
 20 25

## (2) INFORMATION FOR SEQ ID NO:28:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (v) FRAGMENT TYPE: N-terminal

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Ser Ile Asn Gly Asn Ala Pro Ala Glu Ile Asp Leu Arg Gln Met Arg  
 1 5 10 15

Thr Val Thr Pro Ile Arg Met Gln  
 20

## (2) INFORMATION FOR SEQ ID NO:29:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (v) FRAGMENT TYPE: N-terminal

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Ala Phe Ser Gly Val Ala Ala Thr Glu Ser Ala Tyr Leu Ala His Arg  
 1 5 10 15

Asn Gln Ser Leu Asp Leu Ala Glu Gln Glu Leu Val Asp  
 20 25

## (2) INFORMATION FOR SEQ ID NO:30:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (v) FRAGMENT TYPE: N-terminal

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Val Ala Ala Thr Glu Ser Ala Tyr Leu Ala His Arg Asn Gln Ser Leu  
 1 5 10 15

Asp Leu Ala Glu Gln Glu Leu Val Asp  
 20 25

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## (2) INFORMATION FOR SEQ ID NO:31:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (v) FRAGMENT TYPE: N-terminal

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

Ala	Phe	Ser	Gly	Val	Ala	Ala	Thr	Glu	Ser	Ala	Tyr	Leu	Ala	His	Arg
1				5					10					15	

Asn	Gln	Ser	Leu	Asp	Leu	Ala	Glu	Gln
			20					25

## (2) INFORMATION FOR SEQ ID NO:32:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (v) FRAGMENT TYPE: N-terminal

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Val	Ala	Ala	Thr	Glu	Ser	Ala	Tyr	Leu	Ala	His	Arg	Asn	Gln	Ser	Leu
1				5					10					15	

Asp	Leu	Ala	Glu	Gln	Glu	Leu	Val	Asp	Cys	Ala	Ser	Gln
			20					25				

## (2) INFORMATION FOR SEQ ID NO:33:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 28 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (v) FRAGMENT TYPE: N-terminal

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Glu	Tyr	Ile	Gln	His	Asn	Gly	Val	Val	Gln	Glu	Ser	Tyr	Tyr	Arg	Tyr
1				5					10					15	

Val	Ala	Arg	Glu	Gln	Cys	Arg	Arg	Pro	Asn	Ala	Gln
			20					25			

## (2) INFORMATION FOR SEQ ID NO:34:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Asp Thr Ile Pro Arg Gly Ile Glu Tyr Ile Gln His Asn Gly Val Val  
 1 5 10 15

Gln Glu Ser Tyr Tyr Arg Tyr Val Ala Arg Glu Gln Ser  
 20 25

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

Gln Ile Tyr Pro Pro Asn Ala Asn Lys Ile Arg Glu Ala Leu Ala Gln  
 1 5 10 15

Thr His Ser Ala Ile Ala Val Ile Ile Gly Ile Lys Asp  
 20 25

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Gln Ile Tyr Pro Pro Asn Ala Asn Lys Ile Arg Glu Ala Leu Ala Gln  
 1 5 10 15

Thr His Ser Ala Ile Ala  
 20

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: N-terminal

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

Ile Ile Gly Ile Lys Asp Leu Asp Ala Phe Arg His Tyr Asp Gly Arg  
 1 5 10 15

Thr Ile Ile Gln Arg Asp Asn Gly Tyr Gln  
 20 25

## (2) INFORMATION FOR SEQ ID NO:38:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (v) FRAGMENT TYPE: N-terminal

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

Arg Asp Asn Gly Tyr Gln Phe Asn Tyr His Ala Val Asn Ile Val Gly  
 1 5 10 15

Tyr Ser Asn Ala Gln Gly Val Asp Tyr  
 20 25

## (2) INFORMATION FOR SEQ ID NO:39:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (v) FRAGMENT TYPE: N-terminal

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

Asn Ile Val Gly Tyr Ser Asn Ala Gln Gly Val Asp Tyr Trp Ile Val  
 1 5 10 15

Arg Asn Ser Trp Asp Thr Asn Trp Gly Asp Asn Gly Tyr  
 20 25

## (2) INFORMATION FOR SEQ ID NO:40:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (v) FRAGMENT TYPE: N-terminal

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

Asn Ile Val Gly Tyr Ser Asn Ala Gln Gly Val Asp Tyr Trp Ile Val  
 1 5 10 15

Arg Asn Ser Trp Asp Thr Asn  
 20

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## (2) INFORMATION FOR SEQ ID NO:41:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (v) FRAGMENT TYPE: N-terminal

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

Asp Gln Val Asp Val Lys Asp Cys Ala Asn His Glu Ile Lys Lys Val  
1                      5                      10                      15  
  
Leu Val Pro Gly  
                    20

## (2) INFORMATION FOR SEQ ID NO:42:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (v) FRAGMENT TYPE: N-terminal

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

His Glu Ile Lys Lys Val Leu Val Pro Gly Cys His Gly Ser Glu Pro  
1                      5                      10                      15  
  
Cys Ile Ile His Arg Gly Lys Pro Phe  
                    20                      25

## (2) INFORMATION FOR SEQ ID NO:43:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (v) FRAGMENT TYPE: N-terminal

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

His Gly Ser Glu Pro Cys Ile Ile His Arg Gly Lys Pro Phe Gln Leu  
1                      5                      10                      15  
  
Glu Ala Val Phe Glu Ala Asn Gln Asn Thr Lys Thr Ala  
                    20                      25

## (2) INFORMATION FOR SEQ ID NO:44:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

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(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

Gln	Leu	Glu	Ala	Val	Phe	Glu	Ala	Asn	Gln	Asn	Thr	Lys	Thr	Ala	Lys
1				5					10					15	

Ile	Glu	Ile	Lys	Ala	Ser	Ile	Asp	Gly
			20					25

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

Lys	Ile	Glu	Ile	Lys	Ala	Ser	Ile	Asp	Gly	Leu	Glu	Val	Asp	Val	Pro
1				5					10					15	

Gly	Ile	Asp	Pro	Asn	Ala	Cys	His	Tyr	Met	Lys
			20					25		

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

Leu	Glu	Val	Asp	Val	Pro	Gly	Ile	Asp	Pro	Asn	Ala	Cys	His	Tyr	Met
1				5					10					15	

Lys	Cys	Pro	Leu	Val	Lys	Gly	Gln	Gln	Tyr
			20					25	

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

Cys	Pro	Leu	Val	Lys	Gly	Gln	Gln	Tyr	Asp	Ile	Lys	Tyr	Thr	Trp	Asn
1				5					10					15	

Val	Pro	Lys	Ile	Ala	Pro	Lys	Ser	Glu	Asn	Val
			20					25		



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## (2) INFORMATION FOR SEQ ID NO:48:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 26 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: N-terminal

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

Asp	Ile	Lys	Tyr	Thr	Trp	Asn	Val	Pro	Lys	Ile	Ala	Pro	Lys	Ser	Glu
1				5					10					15	
Asn	Val	Val	Val	Thr	Val	Lys	Val	Met	Gly						
				20				25							

## (2) INFORMATION FOR SEQ ID NO:49:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 25 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: N-terminal

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

Val	Val	Thr	Val	Lys	Val	Met	Gly	Asp	Asp	Gly	Val	Leu	Ala	Cys	Ala
1				5					10					15	
Ile	Ala	Thr	His	Ala	Lys	Ile	Arg	Asp							
				20				25							

## (2) INFORMATION FOR SEQ ID NO:50:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 26 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: N-terminal

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

Asp	Gln	Val	Asp	Val	Lys	Asp	Cys	Ala	Asn	His	Glu	Ile	Lys	Lys	Val
1				5					10					15	
Leu	Val	Pro	Gly	Cys	His	Gly	Ser	Glu	Pro						
				20				25							

## (2) INFORMATION FOR SEQ ID NO:51:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 26 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: N-terminal

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

Asp	Gln	Val	Asp	Val	Lys	Asp	Glu	Ala	Asn	His	Glu	Ile	Lys	Lys	Val
1				5					10					15	
Leu	Val	Pro	Gly	Cys	His	Gly	Ser	Glu	Pro						
			20					25							

## (2) INFORMATION FOR SEQ ID NO:52:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (v) FRAGMENT TYPE: N-terminal

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

Asp	Gln	Val	Asp	Val	Lys	Asp	Ser	Ala	Asn	His	Glu	Ile	Lys	Lys	Val
1				5					10					15	
Leu	Val	Pro	Gly	Cys	His	Gly	Ser	Glu	Pro						
			20					25							

## (2) INFORMATION FOR SEQ ID NO:53:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (v) FRAGMENT TYPE: N-terminal

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

Asp	Gln	Val	Asp	Val	Lys	Asp	Cys	Ala	Asn	His	Glu	Ile	Lys	Lys	Val
1				5					10					15	
Leu	Val	Pro	Gly	Glu	His	Gly	Ser	Glu	Pro						
			20					25							

## (2) INFORMATION FOR SEQ ID NO:54:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (v) FRAGMENT TYPE: N-terminal

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

Asp	Gln	Val	Asp	Val	Lys	Asp	Cys	Ala	Asn	His	Glu	Ile	Lys	Lys	Val
1				5					10					15	
Leu	Val	Pro	Gly	Ser	His	Gly	Ser	Glu	Pro						
			20					25							

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## (2) INFORMATION FOR SEQ ID NO:55:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 26 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: N-terminal

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

Asp	Gln	Val	Asp	Val	Lys	Asp	Glu	Ala	Asn	His	Glu	Ile	Lys	Lys	Val
1				5					10					15	
Leu	Val	Pro	Gly	Glu	His	Gly	Ser	Glu	Pro						
			20					25							

## (2) INFORMATION FOR SEQ ID NO:56:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 26 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: N-terminal

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

Asp	Gln	Val	Asp	Val	Lys	Asp	Ser	Ala	Asn	His	Glu	Ile	Lys	Lys	Val
1				5					10					15	
Leu	Val	Pro	Gly	Ser	His	Gly	Ser	Glu	Pro						
			20					25							

## (2) INFORMATION FOR SEQ ID NO:57:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: N-terminal

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

Asp	Gln	Val	Asp	Val	Lys	Asp	Glu	Ala	Asn	His	Glu	Ile	Lys	Lys	Val
1				5					10					15	
Leu	Val	Pro	Gly												
			20												

## (2) INFORMATION FOR SEQ ID NO:58:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

Asp	Gln	Val	Asp	Val	Lys	Asp	Ser	Ala	Asn	His	Glu	Ile	Lys	Lys	Val
1				5					10					15	
Leu Val Pro Gly															
20															

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 16 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

His	Glu	Ile	Lys	Lys	Val	Leu	Val	Pro	Gly	Cys	His	Gly	Ser	Glu	Pro
1				5					10					15	

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 16 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

His	Glu	Ile	Lys	Lys	Val	Leu	Val	Pro	Gly	Glu	His	Gly	Ser	Glu	Pro
1				5					10					15	

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 16 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

His	Glu	Ile	Lys	Lys	Val	Leu	Val	Pro	Gly	Ser	His	Gly	Ser	Glu	Pro
1				5					10					15	

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## (2) INFORMATION FOR SEQ ID NO:62:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (v) FRAGMENT TYPE: N-terminal

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

Lys	Pro	Phe	Gln	Leu	Glu	Ala	Val	Phe	Glu	Ala	Asn	Gln	Asn	Thr	Lys
1				5					10					15	
Thr	Ala	Lys	Ile	Glu	Ile	Lys	Ala	Ser	Thr	Asp	Gly				
			20					25							

## (2) INFORMATION FOR SEQ ID NO:63:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (v) FRAGMENT TYPE: N-terminal

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

Gln	Leu	Glu	Ala	Val	Phe	Glu	Ala	Asn	Gln	Asn	Thr	Lys	Thr	Ala	Lys
1				5					10					15	
Ile	Glu	Ile	Lys	Ala	Ser	Ile	Asp	Gly	Leu	Glu	Val				
			20					25							

## (2) INFORMATION FOR SEQ ID NO:64:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (v) FRAGMENT TYPE: N-terminal

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

Phe	Glu	Ala	Asn	Gln	Asn	Thr	Lys	Thr	Ala	Lys	Ile	Glu	Ile	Lys	Ala
1				5					10					15	
Ser	Ile	Asp	Gly	Leu	Glu	Val	Asp	Val	Pro	Gly					
			20					25							

## (2) INFORMATION FOR SEQ ID NO:65:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

Gln Asn Thr Lys Thr Ala Lys Ile Glu Ile Lys Ala Ser Ile Asp Gly  
1 5 10 15  
Leu Glu Val Asp Val Pro Gly  
20

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 26 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(v) FRAGMENT TYPE: N-terminal

Pro Leu Val Lys Gly Gln Gln Tyr Asp Ile Lys Tyr Thr Trp Asn Val  
1 5 10 15  
Pro Lys Ile Ala Pro Lys Ser Glu Asn Val  
20 25

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 26 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(v) FRAGMENT TYPE: N-terminal

Pro Leu Val Lys Gly Gln Gln Tyr Asp Ile Lys Tyr Thr Tyr Asn Val  
1 5 10 15  
Pro Lys Ile Ala Pro Lys Ser Glu Asn Val  
20 25

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 13 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(v) FRAGMENT TYPE: N-terminal

Lys Ser Glu Asn Val Val Val Thr Val Lys Val Met Gly  
1 5 10

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## (2) INFORMATION FOR SEQ ID NO:69:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 23 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: N-terminal

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

Thr Val Lys Val Met Gly Asp Asp Gly Val Leu Ala Cys Ala Ile Ala  
1 5 10 15

Thr His Ala Lys Ile Arg Asp  
20

## (2) INFORMATION FOR SEQ ID NO:70:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 23 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: N-terminal

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

Thr Val Lys Val Met Gly Asp Asp Gly Val Leu Ala Glu Ala Ile Ala  
1 5 10 15

Thr His Ala Lys Ile Arg Asp  
20

## (2) INFORMATION FOR SEQ ID NO:71:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 23 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: N-terminal

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

Thr Val Lys Val Leu Gly Asp Asp Gly Val Leu Ala Ser Ala Ile Ala  
1 5 10 15

Thr His Ala Lys Ile Arg Asp  
20

## (2) INFORMATION FOR SEQ ID NO:72:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 21 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

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(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

Thr	Ser	Ala	Cys	Arg	Ile	Asn	Ser	Val	Asn	Val	Pro	Ser	Glu	Leu	Asp
1				5					10					15	

Leu	Arg	Ser	Leu	Arg
			20	

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

Glu	Leu	Asp	Leu	Arg	Ser	Leu	Arg	Thr	Val	Thr	Pro	Ile	Arg	Met	Gln
1				5					10					15	

Gly	Gly	Cys	Gly	Ser	Cys	Trp	Ala	Phe	Ser	Gly
			20					25		

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: N-terminal



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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

Thr Val Thr Pro Ile Arg Met Gln Gly Gly Cys Gly Ser Cys Trp Ala  
1 5 10 15

Phe Ser Gly Val Ala Ala Thr Glu Ser Ala Tyr Leu Ala  
20 25

## (2) INFORMATION FOR SEQ ID NO:75:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (v) FRAGMENT TYPE: N-terminal

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

Val Ala Ala Thr Glu Ser Ala Tyr Leu Ala Tyr Arg Asn Thr Ser Leu  
1 5 10 15

Asp Leu Ser Glu Gln  
20

## (2) INFORMATION FOR SEQ ID NO:76:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (v) FRAGMENT TYPE: N-terminal

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

Tyr Arg Asn Thr Ser Leu Asp Leu Ser Glu Gln Glu Leu Val Asp Cys  
1 5 10 15

Ala Ser Gln His Gly Cys  
20

## (2) INFORMATION FOR SEQ ID NO:77:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (v) FRAGMENT TYPE: N-terminal

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

Glu Leu Val Asp Cys Ala Ser Gln His Gly Cys His Gly Asp Thr Ile  
 1 5 10 15  
 Pro Arg Gly Ile Glu  
 20

## (2) INFORMATION FOR SEQ ID NO:78:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 28 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: N-terminal

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

Gly Asp Thr Ile Pro Arg Gly Ile Glu Tyr Ile Gln Gln Asn Gly Val  
 1 5 10 15  
 Val Glu Glu Arg Ser Tyr Pro Tyr Val Ala Arg Glu  
 20 25

## (2) INFORMATION FOR SEQ ID NO:79:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 25 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: N-terminal

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

Gln Asn Gly Val Val Glu Glu Arg Ser Tyr Pro Tyr Val Ala Arg Glu  
 1 5 10 15  
 Gln Arg Cys Arg Arg Pro Asn Ser Gln  
 20 25

## (2) INFORMATION FOR SEQ ID NO:80:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 19 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: N-terminal

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

Gln Arg Cys Arg Arg Pro Asn Ser Gln His Tyr Gly Ile Ser Asn Tyr  
 1 5 10 15  
 Cys Gln Ile

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## (2) INFORMATION FOR SEQ ID NO:81:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 22 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: N-terminal

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

His	Tyr	Gly	Ile	Ser	Asn	Tyr	Cys	Gln	Ile	Tyr	Pro	Pro	Asp	Val	Lys
1				5					10					15	
Gln Ile Arg Glu Ala Leu															
20															

## (2) INFORMATION FOR SEQ ID NO:82:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 24 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: N-terminal

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

Tyr	Pro	Pro	Asp	Val	Lys	Gln	Ile	Arg	Glu	Ala	Leu	Phe	Gln	Thr	His
1				5					10					15	
Thr Ala Ile Ala Val Ile Ile Gly															
20															

## (2) INFORMATION FOR SEQ ID NO:83:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 26 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: N-terminal

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

Thr	Gln	Thr	His	Thr	Ala	Ile	Ala	Val	Ile	Ile	Gly	Ile	Lys	Asp	Leu
1				5					10					15	
Arg	Ala	Phe	Gln	His	Tyr	Asp	Gly	Arg	Thr						
			20					25							

(2) INFORMATION FOR SEQ ID NO:84:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 26 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

Ile	Lys	Asp	Leu	Arg	Ala	Phe	Gln	His	Tyr	Asp	Gly	Arg	Thr	Ile	Ile
1				5					10					15	
Gln	His	Asp	Asn	Gly	Tyr	Gln	Pro	Asn	Tyr						
			20					25							

(2) INFORMATION FOR SEQ ID NO:85:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 15 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

Asp	Gly	Arg	Thr	Ile	Ile	Gln	His	Asp	Asn	Gly	Tyr	Gln	Pro	Asn
1				5					10					15

(2) INFORMATION FOR SEQ ID NO:86:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 23 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: N-terminal

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

Ile Ile Gln His Asp Asn Gly Tyr Gln Pro Asn Tyr His Ala Val Asn  
1 5 10 15

Ile Val Gly Tyr Gly Ser Thr  
20

(2) INFORMATION FOR SEQ ID NO:87:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

His Ala Val Asn Ile Val Gly Tyr Gly Ser Thr Gln Gly Asp Asp Tyr  
1 5 10 15

Trp Ile Val Arg Asn Ser  
20

(2) INFORMATION FOR SEQ ID NO:88:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

Gln Gly Asp Asp Tyr Trp Ile Val Arg Asn Ser Trp Asp Thr Thr Trp  
1 5 10 15

Gly Asp Ser Gly Tyr Gly Tyr Phe  
20

(2) INFORMATION FOR SEQ ID NO:89:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: N-terminal

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

Gly	Asp	Ser	Gly	Tyr	Gly	Tyr	Phe	Gln	Ala	Gly	Asn	Asn	Leu	Met	Met
1				5					10					15	
Ile	Glu	Gln	Tyr	Pro	Tyr	Val	Val	Ile	Met						
			20					25							

(2) INFORMATION FOR SEQ ID NO:90:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 29 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

Thr	Ser	Ala	Cys	Arg	Ile	Asn	Ser	Val	Asn	Val	Pro	Ser	Glu	Leu	Asp
1				5					10					15	
Leu	Arg	Ser	Leu	Arg	Thr	Val	Thr	Pro	Ile	Arg	Met	Gln			
			20					25							

(2) INFORMATION FOR SEQ ID NO:91:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 25 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

Arg	Ile	Asn	Ser	Val	Asn	Val	Pro	Ser	Glu	Leu	Asp	Leu	Arg	Ser	Leu
1				5					10					15	
Arg	Thr	Val	Thr	Pro	Ile	Arg	Met	Gln							
			20					25							

(2) INFORMATION FOR SEQ ID NO:92:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 29 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

Ala	Phe	Ser	Gly	Val	Ala	Ala	Thr	Glu	Ser	Ala	Tyr	Leu	Ala	Tyr	Arg
1				5					10					15	
Asn	Thr	Ser	Leu	Asp	Leu	Ser	Glu	Gln	Glu	Leu	Val	Asp			
			20					25							

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## (2) INFORMATION FOR SEQ ID NO:93:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 25 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: N-terminal

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

Val Ala Ala Thr Glu Ser Ala Tyr Leu Ala Tyr Arg Asn Thr Ser Leu  
 1                      5                                      10                                      15

Asp Leu Ser Glu Gln Glu Leu Val Asp  
                     20                                      25

## (2) INFORMATION FOR SEQ ID NO:94:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 29 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: N-terminal

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

Val Ala Ala Thr Glu Ser Ala Tyr Leu Ala Tyr Arg Asn Thr Ser Leu  
 1                      5                                      10                                      15

Asp Leu Ser Glu Gln Glu Leu Val Asp Cys Ala Ser Gln  
                     20                                      25

## (2) INFORMATION FOR SEQ ID NO:95:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 29 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: N-terminal

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

Glu Tyr Ile Gln Gln Asn Gly Val Val Glu Glu Arg Ser Tyr Pro Tyr  
 1                      5                                      10                                      15

Val Ala Arg Glu Gln Arg Cys Arg Arg Pro Asn Ser Gln  
                     20                                      25

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## (2) INFORMATION FOR SEQ ID NO:96:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 29 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: N-terminal

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

```

Asp Thr Ile Pro Arg Gly Ile Glu Tyr Ile Gln Gln Asn Gly Val Val
1           5           10           15
Glu Glu Arg Ser Tyr Pro Tyr Val Ala Arg Glu Gln Arg
          20           25

```

## (2) INFORMATION FOR SEQ ID NO:97:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 29 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: N-terminal

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

```

Gln Ile Tyr Pro Pro Asp Val Lys Gln Ile Arg Glu Ala Leu Thr Gln
1           5           10           15
Thr His Thr Ala Ile Ala Val Ile Ile Gly Ile Lys Asp
          20           25

```

## (2) INFORMATION FOR SEQ ID NO:98:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 22 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: N-terminal

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

```

Gln Ile Tyr Pro Pro Asp Val Lys Gln Ile Arg Glu Ala Leu Thr Gln
1           5           10           15
Thr His Thr Ala Ile Ala
          20

```



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## (2) INFORMATION FOR SEQ ID NO:99:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 26 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: N-terminal

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

Ile	Ile	Gly	Ile	Lys	Asp	Leu	Arg	Ala	Phe	Gln	His	Tyr	Asp	Gly	Arg
1				5					10					15	
Thr	Ile	Ile	Gln	His	Asp	Asn	Gly	Tyr	Gln						
			20					25							

## (2) INFORMATION FOR SEQ ID NO:100:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 25 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: N-terminal

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

His	Asp	Asn	Gly	Tyr	Gln	Pro	Asn	Tyr	His	Ala	Val	Asn	Ile	Val	Gly
1				5				10						15	
Tyr	Gly	Ser	Thr	Gln	Gly	Asp	Asp	Tyr							
			20					25							

## (2) INFORMATION FOR SEQ ID NO:101:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 29 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: N-terminal

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

Asn	Ile	Val	Gly	Tyr	Gly	Ser	Thr	Gln	Gly	Asp	Asp	Tyr	Trp	Ile	Val
1				5					10					15	
Arg	Asn	Ser	Trp	Asp	Thr	Thr	Trp	Gly	Asp	Ser	Gly	Tyr			
			20					25							

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## (2) INFORMATION FOR SEQ ID NO:102:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (v) FRAGMENT TYPE: N-terminal

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

Asn Ile Val Gly Tyr Gly Ser Thr Gln Gly Asp Asp Tyr Trp Ile Val  
 1                      5                      10                      15

Arg Asn Ser Trp Asp Thr Thr  
                     20

## (2) INFORMATION FOR SEQ ID NO:103:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (v) FRAGMENT TYPE: N-terminal

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

Asp Gln Val Asp Val Lys Asp Cys Ala Asn Asn Glu Ile Lys Lys Val  
 1                      5                      10                      15

Met Val Asp Gly  
                     20

## (2) INFORMATION FOR SEQ ID NO:104:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (v) FRAGMENT TYPE: N-terminal

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

Asn Glu Ile Lys Lys Val Met Val Asp Gly Cys His Gly Ser Asp Pro  
 1                      5                      10                      15

Cys Ile Ile His Arg Gly Lys Pro Phe  
                     20                      25

## (2) INFORMATION FOR SEQ ID NO:105:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

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(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

His	Gly	Ser	Asp	Pro	Cys	Ile	Ile	His	Arg	Gly	Lys	Pro	Phe	Thr	Leu	
1				5					10					15		
Glu Ala Leu Phe Asp Ala Asn Gln Asn Thr Lys Thr Ala																
				20					25							

(2) INFORMATION FOR SEQ ID NO:106:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 19 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

His	Arg	Gly	Lys	Pro	Phe	Thr	Leu	Glu	Ala	Leu	Phe	Asp	Ala	Asn	Gln
1				5					10					15	
Asn Thr Lys															

(2) INFORMATION FOR SEQ ID NO:107:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 25 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

Thr	Leu	Glu	Ala	Leu	Phe	Asp	Ala	Asn	Gln	Asn	Thr	Lys	Thr	Ala	Lys	
1				5					10					15		
Ile Glu Ile Lys Ala Ser Leu Asp Gly																
				20					25							

(2) INFORMATION FOR SEQ ID NO:108:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 26 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: N-terminal

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

Gln	Asn	Thr	Lys	Thr	Ala	Lys	Ile	Glu	Ile	Lys	Ala	Ser	Leu	Asp	Gly
1				5					10					15	
Leu	Glu	Ile	Asp	Val	Pro	Gly	Ile	Asp	Thr						
			20				25								

(2) INFORMATION FOR SEQ ID NO:109:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 27 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

Lys	Ile	Glu	Ile	Lys	Ala	Ser	Leu	Asp	Gly	Leu	Glu	Ile	Asp	Val	Pro
1				5					10					15	
Gly	Ile	Asp	Thr	Asn	Ala	Cys	His	Phe	Met	Lys					
			20				25								

(2) INFORMATION FOR SEQ ID NO:110:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 26 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

Leu	Glu	Ile	Asp	Val	Pro	Gly	Ile	Asp	Thr	Asn	Ala	Cys	His	Phe	Met
1				5					10					15	
Lys	Cys	Pro	Leu	Val	Lys	Gly	Gln	Gln	Tyr						
			20				25								

(2) INFORMATION FOR SEQ ID NO:111:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 27 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: N-terminal

:

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

Cys	Pro	Leu	Val	Lys	Gly	Gln	Gln	Tyr	Asp	Ala	Lys	Tyr	Thr	Trp	Asn
1				5					10					15	
Val	Pro	Lys	Ile	Ala	Pro	Lys	Ser	Glu	Asn	Val					
				20				25							

(2) INFORMATION FOR SEQ ID NO:112:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 26 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

Asp	Ala	Lys	Tyr	Thr	Trp	Asn	Val	Pro	Lys	Ile	Ala	Pro	Lys	Ser	Glu
1				5					10					15	
Asn	Val	Val	Val	Thr	Val	Lys	Leu	Val	Gly						
				20				25							

(2) INFORMATION FOR SEQ ID NO:113:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 35 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

Pro	Lys	Ile	Ala	Pro	Lys	Ser	Glu	Asn	Val	Val	Val	Thr	Val	Lys	Leu
1				5					10					15	
Val	Gly	Asp	Asn	Gly	Val	Leu	Ala	Cys	Ala	Ile	Ala	Thr	His	Ala	Lys
			20					25					30		
Ile	Arg	Asp													
		35													

(2) INFORMATION FOR SEQ ID NO:114:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 25 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: N-terminal

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

Val Val Thr Val Lys Leu Val Gly Asp Asn Gly Val Leu Ala Cys Ala  
1 5 10 15

Ile Ala Thr His Ala Lys Ile Arg Asp  
20 25

(2) INFORMATION FOR SEQ ID NO:115:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 28 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

Lys Pro Phe Thr Leu Glu Ala Leu Phe Asp Ala Asn Gln Asn Thr Lys  
1 5 10 15

Thr Ala Lys Ile Glu Ile Lys Ala Ser Leu Asp Gly  
20 25

(2) INFORMATION FOR SEQ ID NO:116:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 28 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

Thr Leu Glu Ala Leu Phe Asp Ala Asn Gln Asn Thr Lys Thr Ala Lys  
1 5 10 15

Ile Glu Ile Lys Ala Ser Leu Asp Gly Leu Glu Ile  
20 25

(2) INFORMATION FOR SEQ ID NO:117:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

His Arg Asn Gln Ser Leu Asp Leu Ala Glu Gln Asp Leu Val Asp Cys  
1 5 10 15

Ala Ser Gln His Gly Cys  
20

(2) INFORMATION FOR SEQ ID NO:118:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 21 amino acids

(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

Asp Leu Val Asp Cys Ala Ser Gln His Gly Cys His Gly Asp Thr Ile  
1 5 10 15

Pro Arg Gly Ile Glu  
20

(2) INFORMATION FOR SEQ ID NO:119:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 29 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

His Gly Ser Glu Pro Cys Ile Ile His Arg Gly Lys Pro Phe Gln Leu  
1 5 10 15

Glu Ala Val Phe Glu Ala Val Gln Asn Thr Lys Thr Ala  
20 25

### Claims

1. An isolated peptide of a protein allergen of the genus Dermatophagoides, said peptide comprising at least one T cell epitope of said protein allergen, said peptide having a positivity index of at least about 150 and mean T cell stimulation index of at least about 4.0 determined in a population of individuals sensitive to said protein allergen.
2. An isolated peptide of claim 1 selected from the group consisting of: DP I-1 (SEQ ID NO: 9); DP I-21.1 (SEQ ID NO: 27); DP I-21.2 (SEQ ID NO: 28); DP I-23.1 (SEQ ID NO: 33); DP I-23.2 (SEQ ID NO: 34); DP I-25.2 (SEQ ID NO: 36); and DP I-26.1 (SEQ ID NO: 37).
3. An isolated peptide of claim 1 selected from the group consisting of DP I-21.2, DP I 23.1, DP I 26.1, DP II-20.6, DP II-22, DP II-25.2 and DF I-22.2 as shown in Figs. 3 and 4.
4. An isolated peptide of claim 1 which does not bind immunoglobulin E specific for a protein allergen of the genus Dermatophagoides in a substantial percentage of individuals sensitive to the protein allergen, or if binding of the peptide to said immunoglobulin E occurs, such binding does not result in release of mediators from mast cells or basophils in a substantial percentage of individuals sensitive to the protein allergen.
5. An isolated peptide of claim 1 which binds immunoglobulin E to a substantially lesser extent than the protein allergen from which the peptide is derived binds said immunoglobulin E.
6. An isolated peptide of claim 2 wherein the population of individuals is at least 9 individuals.
7. An isolated peptide of claim 2 wherein the population of individuals is at least 29 individuals.
8. An isolated peptide of claim 1 which comprises at least two T cell epitopes.



9. An isolated peptide of claim 1 which, when administered to an individual sensitive to house dust mite, induces T cell anergy in the individual or modifies the lymphokine secretion profile of T cells in the individual.

10. All or a portion of an isolated peptide of Der p I comprising at least one T cell epitope of Der p I, said peptide selected from the group consisting of:

- a) DP I-1 (SEQ ID NO: 9);
- b) DP I-2 (SEQ ID NO: 10);
- c) DP I-3 (SEQ ID NO: 11);
- d) DP I-4 (SEQ ID NO: 12);
- e) DP I-11.1 (SEQ ID NO: 13);
- f) DP I-12.1 (SEQ ID NO: 14);
- g) DP I-5 (SEQ ID NO: 15);
- h) DP I-13 (SEQ ID NO: 17);
- i) DP I-14 (SEQ ID NO: 18);
- j) DP I-15 (SEQ ID NO: 19);
- k) DP I-6.1 (SEQ ID NO: 20);
- l) DP I-7.1 (SEQ ID NO: 21);
- m) DP I-8 (SEQ ID NO: 22);
- n) DP I-9 (SEQ ID NO: 23);
- o) DP I-16 (SEQ ID NO: 24);
- p) DP I-10 (SEQ ID NO: 25);
- q) DP I-17 (SEQ ID NO: 26);
- r) DP I-21.1 (SEQ ID NO: 27);
- s) DP I-21.2 (SEQ ID NO: 28);
- t) DP I-22.1 (SEQ ID NO: 29);
- u) DP I-22.2 (SEQ ID NO: 30);
- v) DP I-22.3 (SEQ ID NO: 31);
- w) DP I-22.4 (SEQ ID NO: 32);
- x) DP I-23.1 (SEQ ID NO: 33);
- y) DP I-23.2 (SEQ ID NO: 34);
- z) DP I-25.1 (SEQ ID NO: 35);
- a') DP I-25.2 (SEQ ID NO: 36);
- b') DP I-26.1 (SEQ ID NO: 37);
- c') DP I-27.1 (SEQ ID NO: 38);

- d') DP I-28.1 (SEQ ID NO: 39); and
- e') DP I-28.2 (SEQ ID NO: 40),

wherein said portion of said peptide has a mean T cell stimulation index equivalent to, or greater than the mean T cell stimulation index of said peptide as shown in Fig. 5 and Fig. 13.

11. A portion of an isolated peptide of claim 10 which has a mean T cell stimulation index of at least 4.0.
12. All or a portion of an isolated peptide of claim 10 which does not bind immunoglobulin E specific for Der p I in a substantial percentage of individuals sensitive to Der p I, or if binding of the peptide or portion thereof to said immunoglobulin E occurs, such binding does not result in release of mediators from mast cells or basophils in a substantial percentage of individuals sensitive to Der p I.
13. All or a portion of an isolated peptide of claim 10 which modifies, in an individual sensitive to house dust mite to whom it is administered, the allergic response of the individual to a house dust mite allergen.
14. A portion of an isolated peptide of claim 10 wherein the portion comprises at least 15 amino acid residues.
15. An isolated nucleic acid having a sequence encoding all or a portion of a peptide of claim 10, or the functional equivalent of said nucleic acid sequence.
16. An isolated peptide which is immunologically cross-reactive with antibodies specific for all or a portion of a peptide of claim 10.
17. An isolated peptide which is immunologically cross-reactive with T cells reactive with all or a portion of a peptide of claim 10.
18. An isolated peptide of Der p I having an amino acid sequence substantially corresponding to an amino acid sequence of a peptide selected from the group consisting of:

- a) DP I-1 (SEQ ID NO: 9);

- b) DP I-2 (SEQ ID NO: 10);
- c) DP I-3 (SEQ ID NO: 11);
- d) DP I-4 (SEQ ID NO: 12);
- e) DP I-11.1 (SEQ ID NO: 13);
- f) DP I-12.1 (SEQ ID NO: 14);
- g) DP I-5 (SEQ ID NO: 15);
- h) DP I-13 (SEQ ID NO: 17);
- i) DP I-14 (SEQ ID NO: 18);
- j) DP I-15 (SEQ ID NO: 19);
- k) DP I-6.1 (SEQ ID NO: 20);
- l) DP I-7.1 (SEQ ID NO: 21);
- m) DP I-8 (SEQ ID NO: 22);
- n) DP I-9 (SEQ ID NO: 23);
- o) DP I-16 (SEQ ID NO: 24);
- p) DP I-10 (SEQ ID NO: 25);
- q) DP I-17 (SEQ ID NO: 26);
- r) DP I-21.1 (SEQ ID NO: 27);
- s) DP I-21.2 (SEQ ID NO: 28);
- t) DP I-22.1 (SEQ ID NO: 29);
- u) DP I-22.2 (SEQ ID NO: 30);
- v) DP I-22.3 (SEQ ID NO: 31);
- w) DP I-22.4 (SEQ ID NO: 32);
- x) DP I-23.1 (SEQ ID NO: 33);
- y) DP I-23.2 (SEQ ID NO: 34);
- z) DP I-25.1 (SEQ ID NO: 35);
- a') DP I-25.2 (SEQ ID NO: 36);
- b') DP I-26.1 (SEQ ID NO: 37);
- c') DP I-27.1 (SEQ ID NO: 38);
- d') DP I-28.1 (SEQ ID NO: 39);
- e') DP I-28.2 (SEQ ID NO: 40); and
- f) DP I-5.1 (SEQ ID NO: 16).

19. An isolated nucleic acid having a sequence encoding a peptide of claim 18, or the functional equivalent of said nucleic acid sequence.

20. An isolated peptide of claim 18 selected from the group consisting of:
- a) DP I-1 (SEQ ID NO: 9);
  - b) DP I-2 (SEQ ID NO: 10);
  - c) DP I-3 (SEQ ID NO: 11);
  - d) DP I-4 (SEQ ID NO: 12);
  - e) DP I-12.1 (SEQ ID NO: 14);
  - f) DP I-5 (SEQ ID NO: 15);
  - g) DP I-6.1 (SEQ ID NO: 20);
  - h) DP I-7.1 (SEQ ID NO: 21);
  - i) DP I-17 (SEQ ID NO: 26);
  - j) DP I-21.1 (SEQ ID NO: 27);
  - k) DP I-21.2 (SEQ ID NO: 28);
  - l) DP I-23.2 (SEQ ID NO: 34);
  - m) DP I-26.1 (SEQ ID NO: 37);
  - n) DP I-27.1 (SEQ ID NO: 38);
  - o) DP I-28.1 (SEQ ID NO: 39); and
  - p) DP I-28.2 (SEQ ID NO: 40).
21. A modified peptide or a modified portion of a peptide of claim 10.
22. A modified peptide of claim 18.
23. A modified peptide of claim 18 selected from the group of peptides consisting of DP I-23.1.1, DP I-23.1.2, DP I-23.1.3, and DP I-23.1.4 as shown in Fig. 28.
24. A modified peptide or a modified portion of a peptide of claim 21 which does not bind immunoglobulin E specific for Der p I in a substantial percentage of individuals sensitive to Der p I, or if binding of the peptide or portion thereof to said immunoglobulin E occurs, such binding does not result in release of mediators from mast cells or basophils in a substantial percentage of individuals sensitive to Der p I.
25. A modified peptide or a modified portion of a peptide of claim 21 which modifies, in an individual sensitive to house dust mite to whom it is

administered, the allergic response of the individual to a house dust mite allergen.

26. An isolated peptide comprising at least two regions, each region comprising at least one T cell epitope of a protein allergen of the genus Dermatophagoides, said regions derived from the same or from different protein allergens of the genus Dermatophagoides, said regions each comprising all or a portion of an amino acid sequence selected from the group consisting of:

- a) DP I-21.1 (SEQ ID NO: 27);
- b) DP I-21.2 (SEQ ID NO: 28);
- c) DP I-22.1 (SEQ ID NO: 29);
- d) DP I-22.2 (SEQ ID NO: 30);
- e) DP I-22.3 (SEQ ID NO: 31);
- f) DP I-22.4 (SEQ ID NO: 32);
- g) DP I-23.1 (SEQ ID NO: 33);
- h) DP I-23.2 (SEQ ID NO: 34);
- i) DP I-25.1 (SEQ ID NO: 35);
- j) DP I-25.2 (SEQ ID NO: 36);
- k) DP I-26.1 (SEQ ID NO: 37);
- l) DP I-27.1 (SEQ ID NO: 38);
- m) DP I-28.1 (SEQ ID NO: 39);
- n) DP I-28.2 (SEQ ID NO: 40);
- o) DP I-1 (SEQ ID NO: 9);
- p) DF I-1 (SEQ ID NO: 72);
- q) DF I-21.1 (SEQ ID NO: 90);
- r) DF I-21.2 (SEQ ID NO: 91);
- s) DF I-22.1 (SEQ ID NO: 92);
- t) DF I-22.2 (SEQ ID NO: 93);
- u) DF I-22.4 (SEQ ID NO: 94);
- v) DF I-23.1 (SEQ ID NO: 95);
- w) DF I-23.2 (SEQ ID NO: 96);
- x) DF I-25.1 (SEQ ID NO: 97);
- y) DF I-25.2 (SEQ ID NO: 98);
- z) DF I-26.1 (SEQ ID NO: 99);
- a') DF I-27.1 (SEQ ID NO: 100);
- b') DF I-28.1 (SEQ ID NO: 101);

c') DF I-28.2 (SEQ ID NO: 102);  
d') DP II-20 (SEQ ID NO: 50);  
e') DP II-20.1 (SEQ ID NO: 51);  
f') DP II-20.2 (SEQ ID NO: 52);  
g') DP II-20.3 (SEQ ID NO: 53);  
h') DP II-20.4 (SEQ ID NO: 54);  
i') DP II-20.5 (SEQ ID NO: 55);  
j') DP II 20.6 (SEQ ID NO: 56);  
k') DP II-1 (SEQ ID NO: 41);  
l') DP II-1.1 (SEQ ID NO: 57);  
m') DP II-1.2 (SEQ ID NO: 58);  
n') DP II-2.1 (SEQ ID NO: 59);  
o') DP II-2.2 (SEQ ID NO: 60);  
p') DP II-2.3 (SEQ ID NO: 61);  
q') DP II-21 (SEQ ID NO: 62);  
r') DP II-22 (SEQ ID NO: 63);  
s') DP II-26 (SEQ ID NO: 64);  
t') DP II-26.1 (SEQ ID NO: 65);  
u') DP II-23 (SEQ ID NO: 66);  
v') DP II-23.1 (SEQ ID NO: 67);  
w') DP II-24 (SEQ ID NO: 68);  
x') DP II-25 (SEQ ID NO: 69);  
y') DP II-25.1 (SEQ ID NO: 70);  
z') DP II-25.2 (SEQ ID NO: 71);  
a'') DF II-1 (SEQ ID NO: 103)  
b'') DF II-2 (SEQ ID NO: 104);  
c'') DF II-13.1 (SEQ ID NO: 105);  
d'') DF II-3.1 (SEQ ID NO: 106);  
e'') DF II-4.5 (SEQ ID NO: 107);  
f'') DF II-4.3 (SEQ ID NO: 108);  
g'') DF II-15 (SEQ ID NO: 109);  
h'') DF II-16 (SEQ ID NO: 110);  
i'') DF II-17 (SEQ ID NO: 111);  
j'') DF II-18 (SEQ ID NO: 112);  
k'') DF II-19 (SEQ ID NO: 113);  
l'') DF II-19.1 (SEQ ID NO: 114);  
m'') DF II-21 (SEQ ID NO: 115); and

n") DF II-22 (SEQ ID NO: 116).

27. An isolated peptide of claim 26 wherein said regions comprise an amino acid sequence selected from the group consisting of:

- a) DP I-21.1 (SEQ ID NO: 27);
- b) DP I-21.2 (SEQ ID NO: 28);
- c) DP I-22.1 (SEQ ID NO: 29);
- d) DP I-23.1 (SEQ ID NO: 33);
- e) DP I-25.2 (SEQ ID NO: 36);
- f) DP I-26.1 (SEQ ID NO: 37);
- g) DP I-28.1 (SEQ ID NO: 39);
- h) DP I-1 (SEQ ID NO: 9);
- i) DF I-1 (SEQ ID NO: 72);
- j) DF I-21.1 (SEQ ID NO: 90);
- k) DF I-22.1 (SEQ ID NO: 92);
- l) DF I-23.1 (SEQ ID NO: 95);
- m) DF I-25.1 (SEQ ID NO: 97);
- n) DP II-1 (SEQ ID NO: 41);
- o) DP II-1.2 (SEQ ID NO: 58);
- p) DP II-2.0 (SEQ ID NO: 56);
- q) DP II-20.3 (SEQ ID NO: 53);
- r) DP II-21 (SEQ ID NO: 62);
- s) DP II-22 (SEQ ID NO: 63);
- t) DP II-25 (SEQ ID NO: 69);
- u) DP II-25.2 (SEQ ID NO: 71);
- v) DF II-2 (SEQ ID NO: 104);
- w) DF II-4.5 (SEQ ID NO: 107);
- x) DF II-15 (SEQ ID NO: 109);
- y) DF II-17 (SEQ ID NO: 111);
- z) DF II-19.1 (SEQ ID NO: 114)
- a') DFI-22.2 (SEQ ID NO:93); and
- b') DP II-20.6 (SEQ ID NO:56).

28. An isolated peptide of claim 26 wherein said regions comprise all or a portion of an amino acid sequence selected from the group consisting of:

- a) DP I-21.2 (SEQ ID NO:27);
- b) DP I-23.1 (SEQ ID NO:33);

- c)DP I-26.1 (SEQ ID NO:37);
- d)DP II-20.6(SEQ ID NO:56);
- e)DP II-22 (SEQ ID NO:63);
- f)DP II-25.2 (SEQ ID NO:71); and
- g)DF I-22.2 (SEQ ID NO:93).

all as shown in Figs. 3 and 4.

29. An isolated peptide of claim 26 wherein said regions comprise an amino acid sequence selected from the group consisting of:

- a)DP I-21.2 (SEQ ID NO:27);
- b)DP I-23.1 (SEQ ID NO:33);
- c)DP I-26.1 (SEQ ID NO:37);
- d)DP II-20.6(SEQ ID NO:56);
- e)DP II-22 (SEQ ID NO:63);
- f)DP II-25.2 (SEQ ID NO:71); and
- g)DF I-22.2 (SEQ ID NO:93), all as shown in Figs. 3 and 4.

30. An isolated peptide of claim 26, wherein said peptide comprises a combination of regions selected from the group consisting of:

- a) DP I-22.1 (SEQ ID NO: 29) and DP I-25.1 (SEQ ID NO: 35);
- b) DP I-21.1 (SEQ ID NO: 27) and DP I-25.2 (SEQ ID NO: 36);
- c) DP I-22.1 (SEQ ID NO: 29) and DP I-1 (SEQ ID NO: 9);
- d) DP I-21.1 (SEQ ID NO: 27), DP I-22.1 (SEQ ID NO: 29), and DP I-25.2 (SEQ ID NO: 36);
- e) DP I-21.2 (SEQ ID NO: 28), DP I-22.1 (SEQ ID NO: 29), and DP I-23.1 (SEQ ID NO: 39);
- f) DP I-1 (SEQ ID NO: 9), DP I-22.1 (SEQ ID NO: 29), and DP I-23.1 (SEQ ID NO: 33);
- g) DP I-1 (SEQ ID NO: 9), DP I-22.1 (SEQ ID NO: 29), and DP I-25.2 (SEQ ID NO: 36);
- h) DP I-21.1 (SEQ ID NO: 27), DP I-22.1



- (SEQ ID NO: 29), DP I-23.1 (SEQ ID NO: 33), and DP I-25.2 (SEQ ID NO: 36);
- i) DP I-21.2 (SEQ ID NO: 28), DP I-22.1 (SEQ ID NO: 29), and DP I-25.2 (SEQ ID NO: 36);
- j) DP I-21.2 (SEQ ID NO: 27), DP I-22.1 (SEQ ID NO: 29), DP I-25.2 (SEQ ID NO: 36), and DP I-26.1 (SEQ ID NO: 37);
- k) DF I-21.2 (SEQ ID NO: 91) and DF I-22.1 (SEQ ID NO: 92);
- l) DF I-21.1 (SEQ ID NO: 90), DF I-22.1 (SEQ ID NO: 92), and DF I-25.1 (SEQ ID NO: 97);
- m) DF I-21.2 (SEQ ID NO: 91), DF I-22.1 (SEQ ID NO: 92), and DF I-25.1 (SEQ ID NO: 97);
- n) DF I-1 (SEQ ID NO: 72) and DF I-22.1 (SEQ ID NO: 92);
- o) DF I-1 (SEQ ID NO: 72), DF I-22.1 (SEQ ID NO: 92), and DF I-25.1 (SEQ ID NO: 97);
- p) DF I-22.1 (SEQ ID NO: 29), and DF I-25.1 (SEQ ID NO: 35);
- q) DF I-21.1 (SEQ ID NO: 90), DF I-22.1 (SEQ ID NO: 92), and DF I-23.1 (SEQ ID NO: 95);
- r) DP I-21.1 (SEQ ID NO: 27), and DF I-22.1 (SEQ ID NO: 92);
- s) DP I-1 (SEQ ID NO: 9), DP I-23.1 (SEQ ID NO: 33), DP I-25.1 (SEQ ID NO: 35), and DF I-1 (SEQ ID NO: 72);
- t) DP I-1 (SEQ ID NO: 9), DP I-25.1 (SEQ ID NO: 35), DP I-23.1 (SEQ ID NO: 33), and DF I-21.2 (SEQ ID NO: 91);
- u) DP I-1 (SEQ ID NO: 9), DP I-25.1 (SEQ ID NO: 35), DP I-23.1 (SEQ ID NO: 33), and DF I-21.1 (SEQ ID NO: 90);
- v) DP II-22 (SEQ ID NO: 63), and DP II-25.2

(SEQ ID NO: 71);

w) DP II-22 (SEQ ID NO: 63), DP II-25.2 (SEQ ID NO: 71), and DP I-21.1 (SEQ ID NO: 27) and DP I-22.1 (SEQ ID NO: 29);

x) DP II-22 (SEQ ID NO: 63), DP II-25.2 (SEQ ID NO: 71), DP II-20.6 (SEQ ID NO: 56), DP I-22.1 (SEQ ID NO: 29), DP I-21.1 (SEQ ID NO: 27), and DP I-23.1 (SEQ ID NO: 33);

y) DP II-22 (SEQ ID NO: 63), DP II-25.2 (SEQ ID NO: 71), DP II-20.6 (SEQ ID NO: 56), DP I-21.1 (SEQ ID NO: 27), DP I-22.1 (SEQ ID NO: 29), and DP I-25.2 (SEQ ID NO: 36);

z) DP II-22 (SEQ ID NO: 63), DP II-25.2 (SEQ ID NO: 71), DP I-21.1 (SEQ ID NO: 27), DP I-22.1 (SEQ ID NO: 29), and DP I-25.2 (SEQ ID NO: 36);

a') DP II-22 (SEQ ID NO: 63), DP II-25.2 (SEQ ID NO: 71), DP I-21.1 (SEQ ID NO: 27), DP I-22.1 (SEQ ID NO: 29), and DP I-23.1 (SEQ ID NO: 33);

b') DP II-22 (SEQ ID NO: 63), DP II-25.2 (SEQ ID NO: 71), DP I-1 (SEQ ID NO: 9), and DP I-22.1 (SEQ ID NO: 29);

c') DF II-4.5 (SEQ ID NO: 107) and DF II-2 (SEQ ID NO: 104);

d') DF II-4.5 (SEQ ID NO: 107) and DF II-19.1 (SEQ ID NO: 114);

e') DF II-4.5 (SEQ ID NO: 107), DF II-2 (SEQ ID NO: 104), and DF II-19.1 (SEQ ID NO: 114);

f') DF II-4.5 (SEQ ID NO: 107), DF II-2 (SEQ ID NO: 104), and DF II-9 (SEQ ID NO: 86);

g') DF II-4.5 (SEQ ID NO: 107); and DF I-21.1 (SEQ ID NO: 90);

h') DF II-4.5 (SEQ ID NO: 107), DP II-22 (SEQ ID NO: 63), and DP II-25.2 (SEQ ID

NO: 71); and

i) DF II-4.5 (SEQ ID NO: 107), DF II-2 (SEQ ID NO: 104), and DP II-22 (SEQ ID NO: 63).

31. An isolated peptide of claim 26 wherein said peptide comprises the following combination of regions: DP I-21.2(SEQ ID NO:27), DP I-23.1(SEQ ID NO:33), DP I-26.1 (SEQ ID NO:37), DP II-20.6(SEQ ID NO:56), DP II-22(SEQ ID NO:63), DP II-25.2(SEQ ID NO:71), and DF I-22.2(SEQ ID NO:93).

32. An isolated nucleic acid having a sequence encoding all or a portion of a peptide of claim 28, or the functional equivalent of said nucleic acid sequence.

33. An isolated peptide produced in a host cell transformed with the nucleic acid of claim 32.

34. An isolated peptide of claim 26 wherein said peptide has a specific sequential arrangement of amino acid sequences, said arrangement of amino acid sequences selected from the group consisting of:

- a) DP I-26.1, DP II-25.2, DF I-22, DP II-20.6 and DPI-21.2 respectively as shown in Fig.25;
- b) DP II-25.2, DF I-22.2, DP I-23.1 DP II-22, DP I-26.1 DPI-21.2 and DP II-20.6 respectively as shown in Fig. 26; and
- c) DP II-25.2, DP I-21.1, DP I-26.1, DP II-22, DP II-20.6 and DF I-22.2 respectively as shown in Fig. 27.

35. An isolated peptide of claim 26 wherein the regions comprise an amino acid sequence selected from the group consisting of:

- a) DP I-21.1 (SEQ ID NO: 27);
- b) DP I-21.2 (SEQ ID NO: 28);
- c) DP I-22.1 (SEQ ID NO: 29);
- d) DP I-22.2 (SEQ ID NO: 30);
- e) DP I-22.3 (SEQ ID NO: 31);
- f) DP I-22.4 (SEQ ID NO: 32);
- g) DP I-23.1 (SEQ ID NO: 33);
- h) DP I-23.2 (SEQ ID NO: 34);

- i) DP I-25.1 (SEQ ID NO: 35);
- j) DP I-25.2 (SEQ ID NO: 36);
- k) DP I-26.1 (SEQ ID NO: 37);
- l) DP I-27.1 (SEQ ID NO: 38);
- m) DP I-28.1 (SEQ ID NO: 39);
- n) DP I-28.2 (SEQ ID NO: 40);
- o) DP I-1 (SEQ ID NO: 9);
- p) DF I-1 (SEQ ID NO: 72);
- q) DF I-21.1 (SEQ ID NO: 90);
- r) DF I-21.2 (SEQ ID NO: 91);
- s) DF I-22.1 (SEQ ID NO: 92);
- t) DF I-22.2 (SEQ ID NO: 93);
- u) DF I-22.4 (SEQ ID NO: 94);
- v) DF I-23.1 (SEQ ID NO: 95);
- w) DF I-23.2 (SEQ ID NO: 96);
- x) DF I-25.1 (SEQ ID NO: 97);
- y) DF I-25.2 (SEQ ID NO: 98);
- z) DF I-26.1 (SEQ ID NO: 99);
- a') DF I-27.1 (SEQ ID NO: 100);
- b') DF I-28.1 (SEQ ID NO: 101);
- c') DF I-28.2 (SEQ ID NO: 102);
- d') DP II-20 (SEQ ID NO: 50);
- e') DP II-20.1 (SEQ ID NO: 51);
- f') DP II-20.2 (SEQ ID NO: 52);
- g') DP II-20.3 (SEQ ID NO: 53);
- h') DP II-20.4 (SEQ ID NO: 54);
- i') DP II-20.5 (SEQ ID NO: 55);
- j') DP II 20.6 (SEQ ID NO: 56);
- k') DP II-1 (SEQ ID NO: 41);
- l') DP II-1.1 (SEQ ID NO: 57);
- m') DP II-1.2 (SEQ ID NO: 58);
- n') DP II-2.1 (SEQ ID NO: 59);
- o') DP II-2.2 (SEQ ID NO: 60);
- p') DP II-2.3 (SEQ ID NO: 61);
- q') DP II-21 (SEQ ID NO: 62);
- r') DP II-22 (SEQ ID NO: 63);
- s') DP II-26 (SEQ ID NO: 64);

- t') DP II-26.1 (SEQ ID NO: 65);
- u') DP II-23 (SEQ ID NO: 66);
- v') DP II-23.1 (SEQ ID NO: 67);
- w') DP II-24 (SEQ ID NO: 68);
- x') DP II-25 (SEQ ID NO: 69);
- y') DP II-25.1 (SEQ ID NO: 70);
- z') DP II-25.2 (SEQ ID NO: 71);
- a'') DF II-1 (SEQ ID NO: 103)
- b'') DF II-2 (SEQ ID NO: 104);
- c'') DF II-13.1 (SEQ ID NO: 105);
- d'') DF II-3.1 (SEQ ID NO: 106);
- e'') DF II-4.5 (SEQ ID NO: 107);
- f'') DF II-4.3 (SEQ ID NO: 108);
- g'') DF II-15 (SEQ ID NO: 109);
- h'') DF II-16 (SEQ ID NO: 110);
- i'') DF II-17 (SEQ ID NO: 111);
- j'') DF II-18 (SEQ ID NO: 112);
- k'') DF II-19 (SEQ ID NO: 113);
- l'') DF II-19.1 (SEQ ID NO: 114)
- m'') DF II-21 (SEQ ID NO: 115); and
- n'') DF II-22 (SEQ ID NO: 116).

36. An isolated nucleic acid having a sequence encoding all or a portion of a peptide of claim 26, or the functional equivalent of said nucleic acid sequence.

37. An isolated peptide produced in a host cell transformed with the nucleic acid of claim 36.

38. All or a portion of an isolated peptide of a protein allergen of the genus Dermatophagoides, said peptide or portion thereof comprising at least one T cell epitope of said protein allergen, said peptide having the formula  $X_n$ -Y- $Z_m$ , wherein Y is an amino acid sequence selected from the group consisting of:

- a) DF I-21.1 (SEQ ID NO: 90);
- b) DF I-21.2 (SEQ ID NO: 91);
- c) DF I-22.1 (SEQ ID NO: 92);

- d) DF I-22.2 (SEQ ID NO: 93);
- e) DF I-22.4 (SEQ ID NO: 94);
- f) DF I-23.1 (SEQ ID NO: 95);
- g) DF I-23.2 (SEQ ID NO: 96);
- h) DF I-25.1 (SEQ ID NO: 97);
- i) DF I-25.2 (SEQ ID NO: 98);
- j) DF I-26.1 (SEQ ID NO: 99);
- k) DF I-27.1 (SEQ ID NO: 100);
- l) DF I-28.1 (SEQ ID NO: 101);
- m) DF I-28.2 (SEQ ID NO: 102);
- n) DF I-1 (SEQ ID NO: 72);
- o) DP II-20 (SEQ ID NO: 50);
- p) DP II-20.1 (SEQ ID NO: 51);
- q) DP II-20.2 (SEQ ID NO: 52);
- r) DP II-20.3 (SEQ ID NO: 53);
- s) DP II-20.4 (SEQ ID NO: 54);
- t) DP II-20.5 (SEQ ID NO: 55);
- u) DP II 20.6 (SEQ ID NO: 56);
- v) DP II-1 (SEQ ID NO: 41);
- w) DP II-1.1 (SEQ ID NO: 57);
- x) DP II-1.2 (SEQ ID NO: 58);
- y) DP II-2.1 (SEQ ID NO: 59);
- z) DP II-2.2 (SEQ ID NO: 60);
- a') DP II-2.3 (SEQ ID NO: 61);
- b') DP II-21 (SEQ ID NO: 62);
- c') DP II-22 (SEQ ID NO: 63);
- d') DP II-26 (SEQ ID NO: 64);
- e') DP II-26.1 (SEQ ID NO: 65);
- f') DP II-23 (SEQ ID NO: 66);
- g') DP II-23.1 (SEQ ID NO: 67);
- h') DP II-24 (SEQ ID NO: 68);
- i') DP II-25 (SEQ ID NO: 69);
- j') DP II-25.1 (SEQ ID NO: 70);
- k') DP II-25.2 (SEQ ID NO: 71);
- l') DP II-1 (SEQ ID NO: 103);
- m') DP II-2 (SEQ ID NO: 104);
- n') DP II-13.1 (SEQ ID NO: 105);

- o') DF II-3.1 (SEQ ID NO: 106);
- p') DF II-4.5 (SEQ ID NO: 107);
- q') DF II-4.3 (SEQ ID NO: 108);
- r') DF II-15 (SEQ ID NO: 109);
- s') DF II-16 (SEQ ID NO: 110);
- t') DF II-17 (SEQ ID NO: 111);
- u') DF II-18 (SEQ ID NO: 112);
- v') DF II-19 (SEQ ID NO: 113);
- w') DF II-19.1 (SEQ ID NO: 114);
- x') DF II-21 (SEQ ID NO: 115); and
- y') DF II-22 (SEQ ID NO: 116).

wherein  $X_n$  are amino acid residues contiguous to the amino terminus of Y in the amino acid sequence of said protein allergen, wherein  $Z_m$  are amino acid residues contiguous to the carboxy terminus of Y in the amino acid sequence of said protein allergen, wherein n is 0-30 and wherein m is 0-30.

39. All or a portion of an isolated peptide of claim 38 wherein  $n=0$  and  $m=0$ .

40. A portion of an isolated peptide of claim 38 wherein the portion comprises at least fifteen amino acid residues.

41. An isolated peptide of claim 38 wherein the peptide comprises up to 45 amino acids.

42. All or a portion of an isolated peptide of claim 38 which does not bind immunoglobulin E specific for a protein allergen of the genus Dermatophagoides in a substantial percentage of individuals sensitive to the protein allergen, or if binding of the peptide or portion thereof to said immunoglobulin E occurs, such binding does not result in release of mediators from mast cells or basophils in a substantial percentage of individuals sensitive to the protein allergen.

43. An isolated peptide of claim 38 which binds immunoglobulin E to a substantially lesser extent than the protein allergen from which the peptide is derived binds said immunoglobulin E.

44. All or a portion of an isolated peptide of a protein allergen of the genus Dermatophagoides, said peptide or portion thereof comprising at least one T cell epitope of said protein allergen, said peptide comprising an amino acid sequence selected from the group consisting of:

- a) DF I-1 (SEQ ID NO: 72);
- b) DF I-2.1 (SEQ ID NO: 73);
- c) DF I-3 (SEQ ID NO: 74);
- d) DF I-4 (SEQ ID NO: 75);
- e) DF I-11 (SEQ ID NO: 76);
- f) DF I-12 (SEQ ID NO: 77);
- g) DF I-5 (SEQ ID NO: 78);
- h) DF I-13 (SEQ ID NO: 79);
- i) DF I-14 (SEQ ID NO: 80);
- j) DF I-15 (SEQ ID NO: 81);
- k) DF I-6 (SEQ ID NO: 82);
- l) DF I-7 (SEQ ID NO: 83);
- m) DF I-8.1 (SEQ ID NO: 84);
- n) DF I-8 (SEQ ID NO: 85);
- o) DF I-9 (SEQ ID NO: 86);
- p) DF I-16 (SEQ ID NO: 87);
- q) DF I-10 (SEQ ID NO: 88);
- r) DF I-17 (SEQ ID NO: 89);
- s) DF I-21.1 (SEQ ID NO: 90);
- t) DF I-21.2 (SEQ ID NO: 91);
- u) DF I-22.1 (SEQ ID NO: 92);
- v) DF I-22.2 (SEQ ID NO: 93);
- w) DF I-22.4 (SEQ ID NO: 94);
- x) DF I-23.1 (SEQ ID NO: 95);
- y) DF I-23.2 (SEQ ID NO: 96);
- z) DF I-25.1 (SEQ ID NO: 97);
- a') DF I-25.2 (SEQ ID NO: 98);
- b') DF I-26.1 (SEQ ID NO: 99);
- c') DF I-27.1 (SEQ ID NO: 100);
- d') DF I-28.1 (SEQ ID NO: 101);
- e') DF I-28.2 (SEQ ID NO: 102);
- f) DP II-20 (SEQ ID NO: 50);
- g') DP II-20.1 (SEQ ID NO: 51);



h') DP II-20.2 (SEQ ID NO: 52);  
i') DP II-20.3 (SEQ ID NO: 53);  
j') DP II-20.4 (SEQ ID NO: 54);  
k') DP II-20.5 (SEQ ID NO: 55);  
l') DP II 20.6 (SEQ ID NO: 56);  
m') DP II-1 (SEQ ID NO: 41);  
o') DP II-2 (SEQ ID NO: 42);  
p') DP II-3.1 (SEQ ID NO: 43);  
q') DP II-4 (SEQ ID NO: 44);  
r') DP II-5 (SEQ ID NO: 45);  
s') DP II-6 (SEQ ID NO: 46);  
t') DP II-7 (SEQ ID NO: 47);  
u') DP II-8 (SEQ ID NO: 48);  
v') DP II-9 (SEQ ID NO: 49);  
w') DP II-1.1 (SEQ ID NO: 57);  
x') DP II-1.2 (SEQ ID NO: 58);  
y') DP II-2.1 (SEQ ID NO: 59);  
z') DP II-2.2 (SEQ ID NO: 60);  
a'') DP II-2.3 (SEQ ID NO: 61);  
b'') DP II-21 (SEQ ID NO: 62);  
c'') DP II-22 (SEQ ID NO: 63);  
d'') DP II-26 (SEQ ID NO: 64);  
e'') DP II-26.1 (SEQ ID NO: 65);  
f'') DP II-23 (SEQ ID NO: 66);  
g'') DP II-23.1 (SEQ ID NO: 67);  
h'') DP II-24 (SEQ ID NO: 68);  
i'') DP II-25 (SEQ ID NO: 69);  
j'') DP II-25.1 (SEQ ID NO: 70);  
k'') DP II-25.2 (SEQ ID NO: 71);  
l'') DF II-1 (SEQ ID NO: 103);  
m'') DF II-2 (SEQ ID NO: 104);  
n'') DF II-13.1 (SEQ ID NO: 105);  
o'') DF II-3.1 (SEQ ID NO: 106);  
p'') DF II-4.5 (SEQ ID NO: 107);  
q'') DF II-4.3 (SEQ ID NO: 108);  
r'') DF II-15 (SEQ ID NO: 109);  
s'') DF II-16 (SEQ ID NO: 110);

- t") DF II-17 (SEQ ID NO: 111);
- u") DF II-18 (SEQ ID NO: 112);
- v") DF II-19 (SEQ ID NO: 113);
- w") DF II-19.1 (SEQ ID NO: 114);
- x") DF II-21 (SEQ ID NO: 115); and
- y") DF II-22 (SEQ ID NO: 116).

45. A portion of an isolated peptide of claim 44 which has a mean T cell stimulation index equivalent to or greater than the mean T cell stimulation index of said peptide as shown in Fig. 10, Fig. 15a and Fig 16a.
46. A portion of an isolated peptide of claim 44 wherein the portion comprises at least fifteen amino acid residues.
47. An isolated peptide of claim 44 wherein the peptide comprises up to 45 amino acids.
48. All or a portion of an isolated peptide of claim 44 which has minimal immunoglobulin E stimulating activity.
49. All or a portion of an isolated peptide of claim 44 which does not bind immunoglobulin E specific for a protein allergen of the genus Dermatophagoides in a substantial percentage of individuals sensitive to the protein allergen or if binding of the peptide or portion thereof to said immunoglobulin E occurs, such binding does not result in release of mediators from mast cells or basophils in a substantial percentage of individuals sensitive to the protein allergen.
50. All or a portion of an isolated peptide of claim 44 which binds immunoglobulin E to a substantially lesser extent than the protein allergen from which the peptide is derived binds said immunoglobulin E.
51. All or a portion of an isolated peptide of claim 44 which modifies, in an individual sensitive to house dust mite to whom it is administered, the allergic response of the individual to a house dust mite allergen.
52. An isolated nucleic acid having a sequence encoding all or a

portion of a peptide of claim 44, or the functional equivalent of said nucleic acid sequence.

53. An isolated peptide which is immunologically cross-reactive with antibodies specific for all or a portion of a peptide of claim 44.

54. An isolated peptide which is immunologically cross-reactive with T cells reactive with all or a portion of a peptide of claim 44.

55. An isolated peptide of a protein allergen of the genus Dermatophagoides, said peptide selected from the group consisting of:

- a) DF I-1 (SEQ ID NO: 72);
- b) DF I-21.1 (SEQ ID NO: 90);
- c) DF I-22.1 (SEQ ID NO: 92);
- d) DF I-25.1 (SEQ ID NO: 97);
- e) DF I-23.1 (SEQ ID NO: 95);
- f) DF I-9 (SEQ ID NO: 86);
- g) DF I-21.2 (SEQ ID NO: 91);
- h) DP II-1 (SEQ ID NO: 41);
- i) DP II-1.2 (SEQ ID NO: 58);
- j) DP II-22 (SEQ ID NO: 63);
- k) DP II-25.1 (SEQ ID NO: 70);
- l) DP II-21 (SEQ ID NO: 62);
- m) DP II-25 (SEQ ID NO: 69);
- n) DP II-20.6 (SEQ ID NO: 56);
- o) DP II-20 (SEQ ID NO: 50);
- p) DF II-4.5 (SEQ ID NO: 107);
- q) DF II-2 (SEQ ID NO: 104);
- r) DF II-19.1 (SEQ ID NO: 114);
- s) DF II-17 (SEQ ID NO: 111);
- t) DF II-15 (SEQ ID NO: 109).
- u) DP II-25.2 (SEQ ID NO: 71); and
- v) DF I-22.2 (SEQ ID NO: 92)

56. A modified peptide or a modified portion of a peptide of claim 44.

57. A modified peptide or a modified portion of a peptide of claim 56 selected from the group of peptides consisting of DP II-22.1 and DP II-22.2 as shown in Fig. 28.

58. A modified peptide or modified portion of a peptide of claim 56 which does not bind immunoglobulin E specific for a protein allergen of the genus Dermatophagoides in a substantial percentage of individuals sensitive to the protein allergen, or if binding of the peptide or portion thereof to said immunoglobulin E occurs, such binding does not result in release of mediators from mast cells or basophils in a substantial percentage of individuals sensitive to the protein allergen.

59. A modified peptide or a modified portion of a peptide of claim 56 which binds immunoglobulin E to a substantially lesser extent than the protein allergen from which the peptide is derived binds said immunoglobulin E.

60. A modified peptide or a modified portion of a peptide of claim 56 which modifies, in an individual sensitive to house dust mite to whom it is administered, the allergic response of the individual to a house dust mite allergen.

61. An isolated peptide of a protein allergen of the genus Dermatophagoides, said peptide selected from the group consisting of:

- a) DF I-1 (SEQ ID NO: 72);
- b) DF I-2.1 (SEQ ID NO: 73);
- c) DF I-3 (SEQ ID NO: 74);
- d) DF I-4 (SEQ ID NO: 75);
- e) DF I-11 (SEQ ID NO: 76);
- f) DF I-12 (SEQ ID NO: 77);
- g) DF I-5 (SEQ ID NO: 78);
- h) DF I-13 (SEQ ID NO: 79);
- i) DF I-14 (SEQ ID NO: 80);
- j) DF I-15 (SEQ ID NO: 81);
- k) DF I-6 (SEQ ID NO: 82);
- l) DF I-7 (SEQ ID NO: 83);
- m) DF I-8.1 (SEQ ID NO: 84);

- n) DF I-8 (SEQ ID NO: 85);
- o) DF I-9 (SEQ ID NO: 86);
- p) DF I-16 (SEQ ID NO: 87);
- q) DF I-10 (SEQ ID NO: 88);
- r) DF I-17 (SEQ ID NO: 89);
- s) DF I-21.1 (SEQ ID NO: 90);
- t) DF I-21.2 (SEQ ID NO: 91);
- u) DF I-22.1 (SEQ ID NO: 92);
- v) DF I-22.2 (SEQ ID NO: 93);
- w) DF I-22.4 (SEQ ID NO: 94);
- x) DF I-23.1 (SEQ ID NO: 95);
- y) DF I-23.2 (SEQ ID NO: 96);
- z) DF I-25.1 (SEQ ID NO: 97);
- a') DF I-25.2 (SEQ ID NO: 98);
- b') DF I-26.1 (SEQ ID NO: 99);
- c') DF I-27.1 (SEQ ID NO: 100);
- d') DF I-28.1 (SEQ ID NO: 101);
- e') DF I-28.2 (SEQ ID NO: 102);
- f) DP II-20 (SEQ ID NO: 50);
- g') DP II-20.1 (SEQ ID NO: 51);
- h') DP II-20.2 (SEQ ID NO: 52);
- i') DP II-20.3 (SEQ ID NO: 53);
- j') DP II-20.4 (SEQ ID NO: 54);
- k') DP II-20.5 (SEQ ID NO: 55);
- l') DP II 20.6 (SEQ ID NO: 56);
- m') DP II-1 (SEQ ID NO: 41);
- o') DP II-2 (SEQ ID NO: 42);
- p') DP II-3.1 (SEQ ID NO: 43);
- q') DP II-4 (SEQ ID NO: 44);
- r') DP II-5 (SEQ ID NO: 45);
- s') DP II-6 (SEQ ID NO: 46);
- t') DP II-7 (SEQ ID NO: 47);
- u') DP II-8 (SEQ ID NO: 48);
- v') DP II-9 (SEQ ID NO: 49);
- w') DP II-1.1 (SEQ ID NO: 57);
- x') DP II-1.2 (SEQ ID NO: 58);
- y') DP II-2.1 (SEQ ID NO: 59);

z') DP II-2.2 (SEQ ID NO: 60);  
a'') DP II-2.3 (SEQ ID NO: 61);  
b'') DP II-21 (SEQ ID NO: 62);  
c'') DP II-22 (SEQ ID NO: 63);  
d'') DP II-26 (SEQ ID NO: 64);  
e'') DP II-26.1 (SEQ ID NO: 65);  
f'') DP II-23 (SEQ ID NO: 66);  
g'') DP II-23.1 (SEQ ID NO: 67);  
h'') DP II-24 (SEQ ID NO: 68);  
i'') DP II-25 (SEQ ID NO: 69);  
j'') DP II-25.1 (SEQ ID NO: 70);  
k'') DP II-25.2 (SEQ ID NO: 71);  
l'') DF II-1 (SEQ ID NO: 103);  
m'') DF II-2 (SEQ ID NO: 104);  
n'') DF II-13.1 (SEQ ID NO: 105);  
o'') DF II-3.1 (SEQ ID NO: 106);  
p'') DF II-4.5 (SEQ ID NO: 107);  
q'') DF II-4.3 (SEQ ID NO: 108);  
r'') DF II-15 (SEQ ID NO: 109);  
s'') DF II-16 (SEQ ID NO: 110);  
t'') DF II-17 (SEQ ID NO: 111);  
u'') DF II-18 (SEQ ID NO: 112);  
v'') DF II-19 (SEQ ID NO: 113);  
w'') DF II-19.1 (SEQ ID NO: 114);  
x'') DF II-21 (SEQ ID NO: 115); and  
y'') DF II-22 (SEQ ID NO: 116).

62. A therapeutic composition comprising at least one isolated peptide of claim 1 and a pharmaceutically acceptable carrier or diluent.

63. A method of treating sensitivity to house dust mite in an individual, comprising administering to the individual a therapeutically effective amount of the composition of claim 62.

64. A method of treating sensitivity to house dust mite in an individual, comprising administering simultaneously or sequentially to the individual a therapeutically effective amount of at least two different

compositions of claim 62.

65. A therapeutic composition comprising at least one isolated peptide of claim 18 and a pharmaceutically acceptable carrier or diluent.

66. A method of treating sensitivity to house dust mite in an individual, comprising administering to the individual a therapeutically effective amount of the composition of claim 65.

67. A therapeutic composition comprising at least one isolated peptide of claim 28 and a pharmaceutically acceptable carrier or diluent

68. A method of treating sensitivity to house dust mite in an individual, comprising administering to the individual a therapeutically effective amount of the composition of claim 67.

69. A therapeutic composition comprising at least one isolated peptide of claim 34 and a pharmaceutically acceptable carrier or diluent.

70. A method of treating sensitivity to house dust mite in an individual, comprising administering to the individual a therapeutically effective amount of the composition of claim 69.

71. A therapeutic composition comprising all or a portion of at least one isolated peptide of claim 38 and a pharmaceutically acceptable carrier or diluent.

72. A method of treating sensitivity to house dust mite in an individual, comprising administering to the individual a therapeutically effective amount of the composition of claim 71.

73. A method of treating sensitivity to house dust mite in an individual, comprising administering simultaneously or sequentially to the individual a therapeutically effective amount of at least two different compositions of claim 71.

74. A therapeutic composition comprising all or a portion of at least one isolated peptide of claim 44 and a pharmaceutically acceptable carrier or diluent.
75. A method of treating sensitivity to house dust mite in an individual, comprising administering to the individual a therapeutically effective amount of the composition of claim 74.
76. A therapeutic composition comprising at least one isolated peptide of claim 61 and a pharmaceutically acceptable carrier or diluent.
77. A method of treating sensitivity to house dust mite in an individual, comprising administering to the individual a therapeutically effective amount of the composition of claim 76.
78. A method of detecting sensitivity to house dust mite in an individual, comprising combining a blood sample obtained from the individual with at least one peptide of claim 1, under conditions appropriate for binding of blood components with the peptide, and determining the extent to which such binding occurs as indicative of sensitivity in the individual to house dust mite.
79. A method of claim 78 wherein the extent to which binding occurs is determined by assessing T cell function, T cell proliferation or a combination thereof.
80. A method of detecting sensitivity to house dust mite in an individual, comprising combining a blood sample obtained from the individual with at least one peptide of claim 18, under conditions appropriate for binding of blood components with the peptide, and determining the extent to which such binding occurs as indicative of sensitivity in the individual to house dust mite.
81. A method of claim 80 wherein the extent to which binding occurs is determined by assessing T cell function, T cell proliferation or a combination thereof.



82. A method of detecting sensitivity to house dust mite in an individual, comprising combining a blood sample obtained from the individual with all or a portion of at least one peptide of claim 38, under conditions appropriate for binding of blood components with the peptide or portion thereof, and determining the extent to which such binding occurs as indicative of sensitivity in the individual to house dust mite.

83. A method of claim 82 wherein the extent to which binding occurs is determined by assessing T cell function, T cell proliferation or a combination thereof.

84. A therapeutic composition comprising a pharmaceutically acceptable carrier or diluent and at least two peptides, said peptides each comprising at least one T cell epitope of a protein allergen of the genus Dermatophagoides, said peptides derived from the same or from different protein allergens of the genus Dermatophagoides.

85. A composition of claim 84 wherein said peptides are selected from the group consisting of:

- a) DP I-21.1 (SEQ ID NO: 27);
- b) DP I-21.2 (SEQ ID NO: 28);
- c) DP I-22.1 (SEQ ID NO: 29);
- d) DP I-22.2 (SEQ ID NO: 30);
- e) DP I-22.3 (SEQ ID NO: 31);
- f) DP I-22.4 (SEQ ID NO: 32);
- g) DP I-23.1 (SEQ ID NO: 33);
- h) DP I-23.2 (SEQ ID NO: 34);
- i) DP I-25.1 (SEQ ID NO: 35);
- j) DP I-25.2 (SEQ ID NO: 36);
- k) DP I-26.1 (SEQ ID NO: 37);
- l) DP I-27.1 (SEQ ID NO: 38);
- m) DP I-28.1 (SEQ ID NO: 39);
- n) DP I-28.2 (SEQ ID NO: 40);
- o) DP I-1 (SEQ ID NO: 9);
- p) DF I-1 (SEQ ID NO: 72);
- q) DF I-21.1 (SEQ ID NO: 90);
- r) DF I-21.2 (SEQ ID NO: 91);

- s) DF I-22.1 (SEQ ID NO: 92);
- t) DF I-22.2 (SEQ ID NO: 93);
- u) DF I-22.4 (SEQ ID NO: 94);
- v) DF I-23.1 (SEQ ID NO: 95);
- w) DF I-23.2 (SEQ ID NO: 96);
- x) DF I-25.1 (SEQ ID NO: 97);
- y) DF I-25.2 (SEQ ID NO: 98);
- z) DF I-26.1 (SEQ ID NO: 99);
- a') DF I-27.1 (SEQ ID NO: 100);
- b') DF I-28.1 (SEQ ID NO: 101);
- c') DF I-28.2 (SEQ ID NO: 102);
- d') DP II-20 (SEQ ID NO: 50);
- e') DP II-20.1 (SEQ ID NO: 51);
- f') DP II-20.2 (SEQ ID NO: 52);
- g') DP II-20.3 (SEQ ID NO: 53);
- h') DP II-20.4 (SEQ ID NO: 54);
- i') DP II-20.5 (SEQ ID NO: 55);
- j') DP II-20.6 (SEQ ID NO: 56);
- k') DP II-1 (SEQ ID NO: 41);
- l') DP II-1.1 (SEQ ID NO: 57);
- m') DP II-1.2 (SEQ ID NO: 58);
- n') DP II-2.1 (SEQ ID NO: 59);
- o') DP II-2.2 (SEQ ID NO: 60);
- p') DP II-2.3 (SEQ ID NO: 61);
- q') DP II-21 (SEQ ID NO: 62);
- r') DP II-22 (SEQ ID NO: 63);
- s') DP II-26 (SEQ ID NO: 64);
- t') DP II-26.1 (SEQ ID NO: 65);
- u') DP II-23 (SEQ ID NO: 66);
- v') DP II-23.1 (SEQ ID NO: 67);
- w') DP II-24 (SEQ ID NO: 68);
- x') DP II-25 (SEQ ID NO: 69);
- y') DP II-25.1 (SEQ ID NO: 70);
- z') DP II-25.2 (SEQ ID NO: 71);
- a'') DF II-1 (SEQ ID NO: 103)
- b'') DF II-2 (SEQ ID NO: 104);
- c'') DF II-13.1 (SEQ ID NO: 105);

- d") DF II-3.1 (SEQ ID NO: 106);
- e") DF II-4.5 (SEQ ID NO: 107);
- f") DF II-4.3 (SEQ ID NO: 108);
- g") DF II-15 (SEQ ID NO: 109);
- h") DF II-16 (SEQ ID NO: 110);
- i") DF II-17 (SEQ ID NO: 111);
- j") DF II-18 (SEQ ID NO: 112);
- k") DF II-19 (SEQ ID NO: 113);
- l") DF II-19.1 (SEQ ID NO: 114)
- m") DF II-21 (SEQ ID NO: 115); and
- n") DF II-22 (SEQ ID NO: 116),

wherein said composition comprises a sufficient percentage of the T cell epitopes of at least one protein allergen such that upon administration of the composition to an individual sensitive to a house dust mite allergen, T cells of the individual are tolerized to said at least one protein allergen.

86. A composition of claim 85 wherein said peptides are selected from the group consisting of :

- a) DP I-21.2 (SEQ ID NO:27);
- b) DP I-23.1 (SEQ ID NO:33);
- c) DP I-26.1 (SEQ ID NO:37);
- d) DP II-20.6 (SEQ ID NO:56);
- e) DP II-22 (SEQ ID NO:63);
- f) DP II-25.2 (SEQ ID NO:71); and
- g) DP I-22.2 (SEQ ID NO:93).

87. A composition of claim 84 comprising a combination of peptides selected from the group consisting of:

- a) DP I-22.1 (SEQ ID NO: 29) and DP I-25.1 (SEQ ID NO: 35);
- b) DP I-21.1 (SEQ ID NO: 27) and DP I-25.2 (SEQ ID NO: 36);
- c) DP I-22.1 (SEQ ID NO: 29) and DP I-1 (SEQ ID NO: 9);
- d) DP I-21.1 (SEQ ID NO: 27), DP I-22.1 (SEQ ID NO: 29), and DP I-25.2 (SEQ ID

NO: 36);

e) DP I-21.2 (SEQ ID NO: 28), DP I-22.1 (SEQ ID NO: 29), and DP I-23.1 (SEQ ID NO: 39);

f) DP I-1 (SEQ ID NO: 9), DP I-22.1 (SEQ ID NO: 29), and DP I-23.1 (SEQ ID NO: 33);

g) DP I-1 (SEQ ID NO: 9), DP I-22.1 (SEQ ID NO: 29), and DP I-25.2 (SEQ ID NO: 36);

h) DP I-21.1 (SEQ ID NO: 27), DP I-22.1 (SEQ ID NO: 29), DP I-23.1 (SEQ ID NO: 33), and DP I-25.2 (SEQ ID NO: 36);

i) DP I-21.2 (SEQ ID NO: 28), DP I-22.1 (SEQ ID NO: 29), and DP I-25.2 (SEQ ID NO: 36);

j) DP I-21.2 (SEQ ID NO: 27), DP I-22.1 (SEQ ID NO: 29), DP I-25.2 (SEQ ID NO: 36), and DP I-26.1 (SEQ ID NO: 37);

k) DF I-21.2 (SEQ ID NO: 91) and DF I-22.1 (SEQ ID NO: 92);

l) DF I-21.1 (SEQ ID NO: 90), DF I-22.1 (SEQ ID NO: 92), and DF I-25.1 (SEQ ID NO: 97);

m) DF I-21.2 (SEQ ID NO: 91), DF I-22.1 (SEQ ID NO: 92), and DF I-25.1 (SEQ ID NO: 97);

n) DF I-1 (SEQ ID NO: 72) and DF I-22.1 (SEQ ID NO: 92);

o) DF I-1 (SEQ ID NO: 72), DF I-22.1 (SEQ ID NO: 92), and DF I-25.1 (SEQ ID NO: 97);

p) DF I-22.1 (SEQ ID NO: 29), and DF I-25.1 (SEQ ID NO: 35);

q) DF I-21.1 (SEQ ID NO: 90), DF I-22.1 (SEQ ID NO: 92), and DF I-23.1 (SEQ ID NO: 95);

r) DP I-21.1 (SEQ ID NO: 27), and DF I-22.1 (SEQ ID NO: 92);

s) DP I-1 (SEQ ID NO: 9), DP I-23.1 (SEQ ID

NO: 33), DP I-25.1 (SEQ ID NO: 35), and  
DF I-1 (SEQ ID NO: 72);

t) DP I-1 (SEQ ID NO: 9), DP I-25.1 (SEQ ID  
NO: 35), DP I-23.1 (SEQ ID NO: 33), and  
DF I-21.2 (SEQ ID NO: 91);

u) DP I-1 (SEQ ID NO: 9), DP I-25.1 (SEQ ID  
NO: 35), DP I-23.1 (SEQ ID NO: 33), and  
DF I-21.1 (SEQ ID NO: 90);

v) DP II-22 (SEQ ID NO: 63), and DP II-25.2  
(SEQ ID NO: 71);

w) DP II-22 (SEQ ID NO: 63), DP II-25.2  
(SEQ ID NO: 71), and DP I-21.1 (SEQ ID  
NO: 27) and DP I-22.1 (SEQ ID NO: 29);

x) DP II-22 (SEQ ID NO: 63), DP II-25.2  
(SEQ ID NO: 71), DP II-20.6 (SEQ ID NO:  
56), DP I-22.1 (SEQ ID NO: 29), DP I-21.1  
(SEQ ID NO: 27), and DP I-23.1 (SEQ ID  
NO: 33);

y) DP II-22 (SEQ ID NO: 63), DP II-25.2  
(SEQ ID NO: 71), DP II-20.6 (SEQ ID NO:  
56), DP I-21.1 (SEQ ID NO: 27), DP I-22.1  
(SEQ ID NO: 29), and DP I-25.2 (SEQ ID  
NO: 36);

z) DP II-22 (SEQ ID NO: 63), DP II-25.2  
(SEQ ID NO: 71), DP I-21.1 (SEQ ID NO:  
27), DP I-22.1 (SEQ ID NO: 29), and DP I-  
25.2 (SEQ ID NO: 36);

a') DP II-22 (SEQ ID NO: 63), DP II-25.2  
(SEQ ID NO: 71), DP I-21.1 (SEQ ID NO:  
27), DP I-22.1 (SEQ ID NO: 29), and DP I-  
23.1 (SEQ ID NO: 33);

b') DP II-22 (SEQ ID NO: 63), DP II-25.2  
(SEQ ID NO: 71), DP I-1 (SEQ ID NO: 9),  
and DP I-22.1 (SEQ ID NO: 29);

c') DF II-4.5 (SEQ ID NO: 107) and DF II-2  
(SEQ ID NO: 104);

d') DF II-4.5 (SEQ ID NO: 107) and DF II-19.1

- (SEQ ID NO: 114);
- e') DF II-4.5 (SEQ ID NO: 107), DF II-2 (SEQ ID NO: 104), and DF II-19.1 (SEQ ID NO: 114);
- f') DF II-4.5 (SEQ ID NO: 107), DF II-2 (SEQ ID NO: 104), and DF II-9 (SEQ ID NO: 86);
- g') DF II-4.5 (SEQ ID NO: 107); and DF I-21.1 (SEQ ID NO: 90);
- h') DF II-4.5 (SEQ ID NO: 107), DP II-22 (SEQ ID NO: 63), and DP II-25.2 (SEQ ID NO: 71); and
- i') DF II-4.5 (SEQ ID NO: 107), DF II-2 (SEQ ID NO: 104), and DP II-22 (SEQ ID NO: 63).

88. A composition of claim 85 comprising the following combination of peptides: DP I-21.2(SEQ ID NO:27),DP I-23.1(SEQ ID NO:33), DP I-26.1 (SEQ ID NO:37), DP II-20.6(SEQ ID NO:56), DP II-22(SEQ ID NO:63), DP II-25.2(SEQ ID NO:71), and DF I-22.2(SEQ ID NO:93).

89. A method of treating sensitivity to house dust mite in an individual, comprising administering to the individual a therapeutically effective amount of the composition of claim 84.

90. A method of treating sensitivity to house dust mite in an individual, comprising administering to the individual a therapeutically effective amount of the composition of claim 85.

91. A method of treating sensitivity to house dust mite in an individual, comprising administering to the individual a therapeutically effective amount of the composition of claim 86.

92. A method of treating sensitivity to house dust mite in an individual, comprising administering to the individual a therapeutically effective amount of the composition of claim 88.

93. A therapeutic composition comprising at least one peptide of at least one protein allergen of the genus Dermatophagoides and a pharmaceutically acceptable carrier or diluent, said composition comprising a

sufficient percentage of the T cell epitopes of said at least one protein allergen such that upon administration of the composition to an individual sensitive to a house dust mite allergen, T cells of the individual are tolerized to said at least one protein allergen.

94. A therapeutic composition of claim 93 wherein said protein allergen is selected from the group consisting of: Der p I; Der f I; Der p II; and Der f II.

95. A method of treating sensitivity to house dust mite in an individual, comprising administering to the individual a therapeutically effective amount of a composition of claim 93.

96. A modified peptide of claim 21 or 56 wherein at least one of the amino acid residues which bind the MHC protein complex but is not essential for such binding is substituted.

97. A modified peptide of claim 96 wherein said amino acid residues are substituted with amino acids selected from the group consisting of alanine, glutamic acid, and a methyl amino acid.

98. The modified peptide of claim 96 wherein at least one of the amino acid residues which is essential for binding to the MHC protein complex is substituted with a conservative amino acid residue.

99. A modified peptide of claim 21 or 56 wherein at least one of the amino acid residues which binds to the T cell receptor, but is not essential for such binding is substituted.

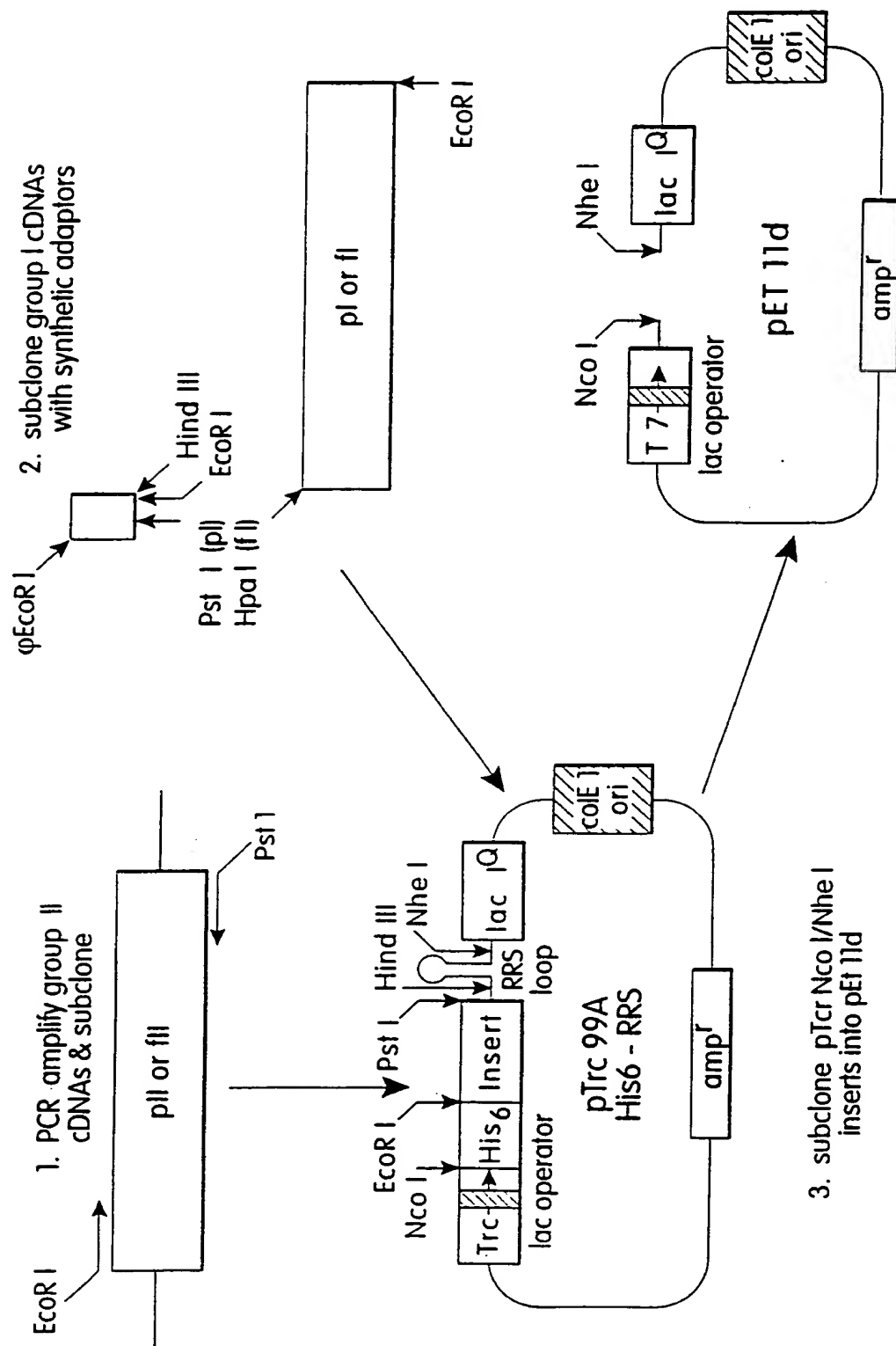


Fig. 1



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Der fI adaptor  
 T S A C R I N S V N  
 5' -AATTACCTCTGCTTGCCGTATCAACTCTGTAAACGCGGAATTCA-3' Hind III  
 φEcor I 3' -ATGGAGACGAACGGCATAGTTGAGACAAATTGCGCCCTTAAGTTCGA-5'  
 Hpa I Ecor I

Der pI adaptor  
 T N A C S  
 5' -AATTACCAACGCCCTGCAGGCGAAGAATTCA-3' Hind III  
 φEcor I 3' -ATGGTTGCGGACGTCGCTTCTTAAGTTCGA-5'  
 Pst I Ecor I

Fig. 2a

5' Der fII/pII primer  
 5' -GGGAATTTCGATCAAGTCGATGTCAA-3'  
 3' fII/pII primer  
 5' -GGCTGCAGTTATATTTAATCGCGGATTTT-3'

Der fII mutagenesis primer  
 5' -AATTGAAATCAAAGCCA-3'

Fig. 2b

Peptide Name	
DPI-1(1-20)	TNAC
DPI-2(13-39)	IDL
DPI-3(21-49)	TVTP
DPI-4(40-60)	VAA
DPI-11.1(50-71)	HRNQ
DPI-12.1(61-81)	ELVD
DPI-5(73-100)	GDTI
DPI-5.1(81-100)	EYIQ
DPI-13(85-109)	HNGV
DPI-14(101-119)	QSCR
DPI-15(110-131)	RFGI
DPI-6.1(120-143)	YPPN
DPI-7.1(132-157)	AQTH
DPI-8(144-169)	IKDL
DPI-9(158-180)	IIQR
DPI-16(170-191)	HAVN
DPI-10(181-204)	QGV
DPI-17(197-222)	GDNG
DPI-21.1(1-28)	TNAC
DPI-21.2(5-28)	SING
DPI-22.1(36-64)	AFSG
DPI-22.2(40-64)	VAA
DPI-22.3(36-60)	AFSG
DPI-22.4(40-68)	VAA
DPI-23.1(81-109)	EYIQ
DPI-23.2(74-102)	DTIP
DPI-25.1(118-146)	QIYP

TNAC  
 EIDL  
 TVTP  
 VAA  
 HRNQ  
 ELVD  
 GDTI  
 EYIQ  
 HNGV  
 QSCR  
 RFGI  
 YPPN  
 AQTH  
 IKDL  
 IIQR  
 HAVN  
 QGV  
 GDNG  
 TNAC  
 SING  
 AFSG  
 VAA  
 AFSG  
 VAA  
 EYIQ  
 DTIP  
 QIYP

Fig. 3

DPI-25.2(118-139)	QIYPPNANKIREALAQTHSAIA
DPI-26.1(141-166)	IIGIKDLDAFRHYDGRITIQRDNGYQ
DPI-27.1(161-185)	RDNGYQPNYHAVNIVGYSNAQGVDY
DPI-28.1(173-201)	NIVGYSNAQGVDYWIVRNSWDTNWGDNGY
DPI-28.2(173-195)	NIVGYSNAQGVDYWIVRNSWDTN
DPII-1(1-20)	DQVDVKDCANHEIKKVLVPG
DPII-2(11-35)	HEIKKVLVPGCHGSEPCIHRGKPF
DPII-3.1(22-50)	HGSEPCIHRGKPFQLEAVFEANQNTKTA
DPII-4(36-60)	QLEAVFEANQNTKTAKEIKASIDG
DPII-5(51-77)	KIEIKASIDGLEVDVPGIDPNACHYMK
DPII-6(61-86)	LEVDPGIDPNACHYMKCPLVKGQQY
DPII-7(78-104)	CPLVKGQQYDIKYTWNVPKIAPKSENV
DPII-8(87-112)	DIKYTWNVPKIAPKSENVVTVKVMG
DPII-9(105-129)	VTVKVMGDDGVLACAIATHAKIRD
DPII-20(1-26)	DQVDVKDCANHEIKKVLVPGCHGSEP
DPII-20.1(1-26)E8	DQVDVKDEANHEIKKVLVPGCHGSEP
DPII-20.2(1-26)S8	DQVDVKDSANHEIKKVLVPGCHGSEP
DPII-20.3(1-26)E21	DQVDVKDCANHEIKKVLVPGCHGSEP
DPII-20.4(1-26)S21	DQVDVKDCANHEIKKVLVPGCHGSEP
DPII-20.5(1-26)E8E21	DQVDVKDEANHEIKKVLVPGCHGSEP
DPII-20.6(1-26)S8S21	DQVDVKDSANHEIKKVLVPGCHGSEP

Fig. 3 cont.

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DPII-1.1(1-20)E8	DQVDVKDEANHEIKKVLVPG
DPII-1.2(1-20)S8	DQVDVKDSANHEIKKVLVPG
DPII-2.1(11-26)	HEIKKVLVPGCHGSEP
DPII-2.2(11-26)E21	HEIKKVLVPGEHGSEP
DPII-2.3(11-26)S21	HEIKKVLVPGSHGSEP
DPII-21(33-60)	KPFQLEAVFEANQNTKTAKIEIKASIDG
DPII-22(36-63)	QLEAVFEANQNTKTAKIEIKASIDGLEV
DPII-26(41-67)	FEANQNTKTAKIEIKASIDGLEVDVPG
DPII-26.1(45-67)	QNTKTAKIEIKASIDGLEVDVPG
DPII-23(79-104)	PLVKGQQYDIKYTNVVPKIAPKSENV
DPII-23.1(79-104)Y92	PLVKGQQYDIKYTYNVVPKIAPKSENV
DPII-24(100-112)	KSENVVVTVKVMG
DPII-25(107-129)	TVKVMGDDGVLACAIATHAKIRD
DPII-25.1(107-129)E119	TVKVMGDDGVLAEAIATHAKIRD
DPII-25.2(107-129)L111S119	TVKVLGDDGVLASAIATHAKIRD

Fig. 3 cont.

Peptide Name	
DFI-1(1-20)	TSACRINSVNVPSELDLRSLR
DFI-2.1(13-39)	ELDLRSLRTVTPIRMQGGCGSCWAFSG
DFI-3(21-49)	TVTPIRMQGGCGSCWAFSGVAATESAYLA
DFI-4(40-60)	VAAATESAYLAYRNTSLDLSEQ
DFI-11(50-71)	YRNTSLDLSEQELVDCASQHGHC
DFI-12(61-81)	ELVDCASQHGCHGDTIPRGIE
DFI-5(73-100)	GDTIPRGIEYIQQNGVVEERSYPYVARE
DFI-13(85-109)	QNGVVEERSYPYVAREQRCRRPNSQ
DFI-14(101-119)	QRCRRPNSQHYGISNYCQI
DFI-15(110-131)	HYGISNYCQIYPPDVVKQIREAL
DFI-6(120-143)	YPPDVVKQIREALTQTHTAIAVIG
DFI-7(132-157)	TQTHTAIAVIGIKDLRAFRHYDGRT
DFI-8.1(144-169)	IKDLRAFRHYDGRTIIQHDNGYQPNY
DFI-8(154-168)	DGRTIIQHDNGYQPN
DFI-9(158-180)	IIQHDNGYQPNYHAVNIVGYGST
DFI-16(170-191)	HAVNIVGYGSTQGDDYWIVRNS
DFI-10(181-204)	QGDDYWIVRNSWDTTWGDSGYGYF
DFI-17(197-222)	GDSDGYGYFQAGNNLMMIEQYPYVIM
DFI-21.1(1-28)	TSACRINSVNVPSELDLRSLRTVTPIRMQ
DFI-21.2(5-28)	RINSVNVPSELDLRSLRTVTPIRMQ
DFI-22.1(36-64)	AFSGVAATESAYLAYRNTSLDLSEQELVD
DFI-22.2(40-64)	VAAATESAYLAYRNTSLDLSEQELVD
DFI-22.4(40-68)	VAAATESAYLAYRNTSLDLSEQELVDCASQ
DFI-23.1(81-109)	EYIQQNGVVEERSYPYVAREQRCRRPNSQ
DFI-23.2(74-102)	DTIPRGIEYIQQNGVVEERSYPYVAREQR
DFI-25.1(118-146)	QIYPPDVVKQIREALTQTHTAIAVIGIKD
DFI-25.2(118-139)	QIYPPDVVKQIREALTQTHTAIA
DFI-26.1(141-166)	IIGIKDLRAFRHYDGRTIIQHDNGYQ

Fig. 4

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DFI-27.1(161-185)	HDNGYQPNYHAVNIVGYGSTQGDDY
DFI-28.1(173-201)	NIVGYGSTQGDDYWIVRNSWDTTWGDSGY
DFI-28.2(173-195)	NIVGYGSTQGDDYWIVRNSWDTT
DFII-1(1-20)	DQVDVKDCANNEIKKVMVDG
DFII-2(11-35)	NEIKKVMVDGCHGSDPCIHRGKPF
DFII-13.1(22-50)	HGSDPCIHRGKPF TLEALFDANQNTKTA
DFII-3.1(30-48)	HRGKPF TLEALFDANQNTK
DFII-4.5(36-60)	TLEALFDANQNTAKIEIKASLDG
DFII-4.3(45-70)	QNTKTAKIEIKASLDGLEIDVPGIDT
DFII-15(51-77)	KIEIKASLDGLEIDVPGIDTNACHFMK
DFII-16(61-86)	LEIDVPGIDTNACHFMKCP LVKGQQY
DFII-17(78-104)	CPLVKGQQYDAKYTWNVPKIAPKSENV
DFII-18(87-112)	DAKYTWNVPKIAPKSENVVTVKLVG
DFII-19(95-129)	PKIAPKSENVVTVKLVGDNGVLACAIATHAKIRD
DFII-19.1(105-129)	VVTVKLVGDNGVLACAIATHAKIRD
DFII-21(33-60)	KPFTLEALFDANQNTKTAKIEIKASLDG
DFII-22(36-63)	TLEALFDANQNTKTAKIEIKASLDGLEI

Fig. 4 cont.

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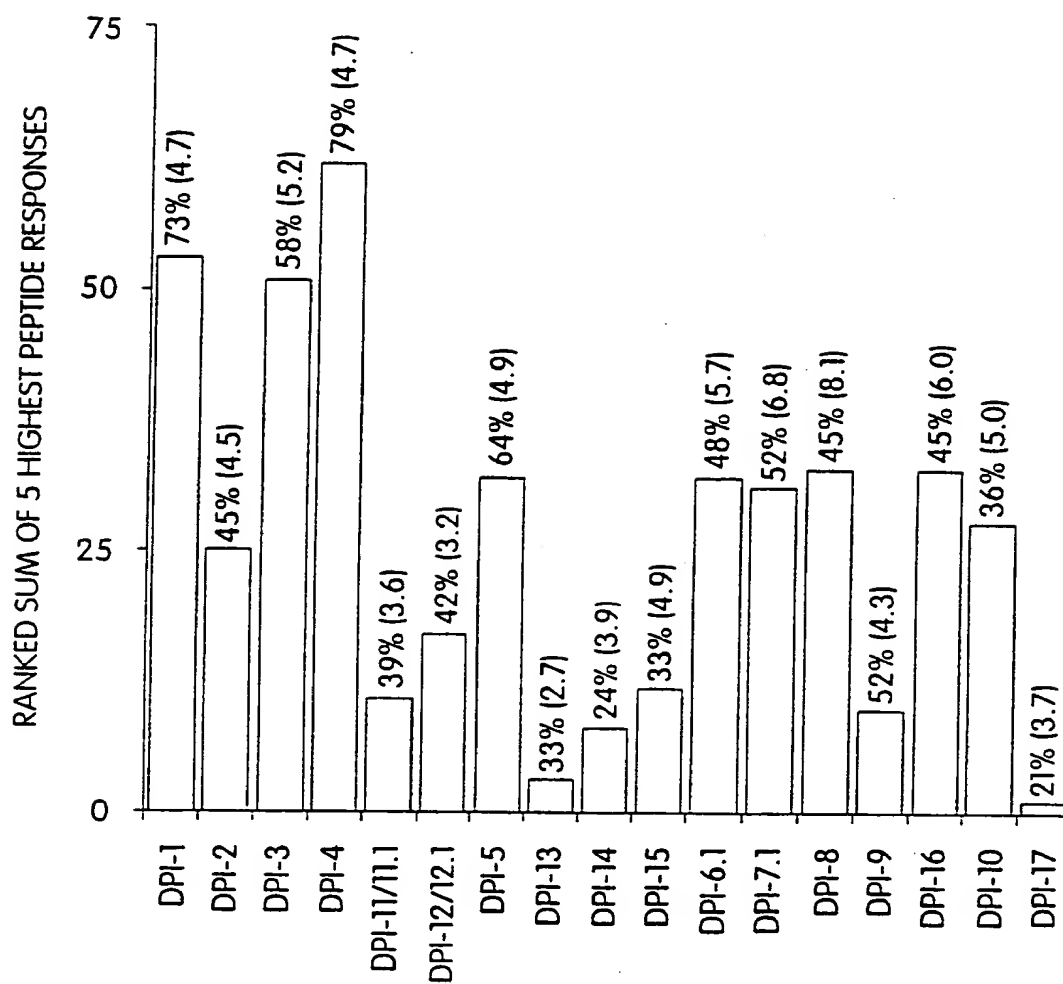


Fig. 5

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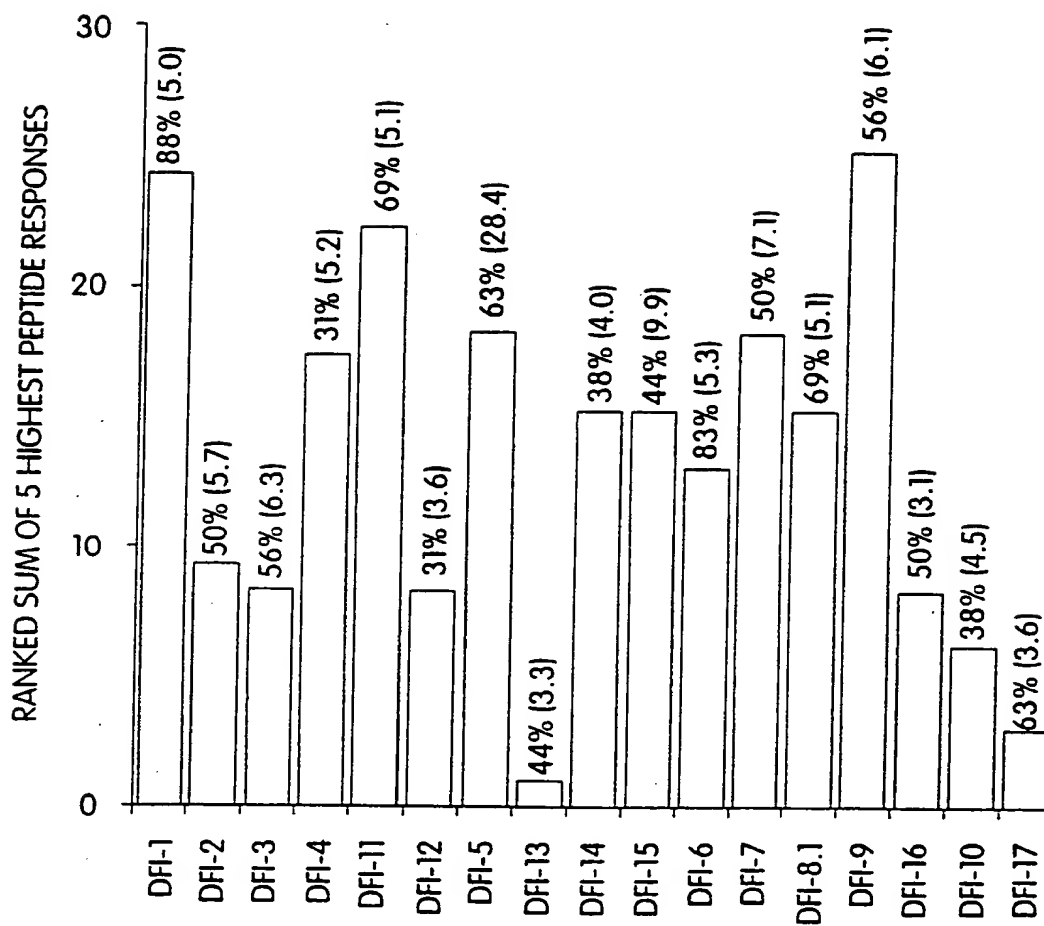


Fig. 6



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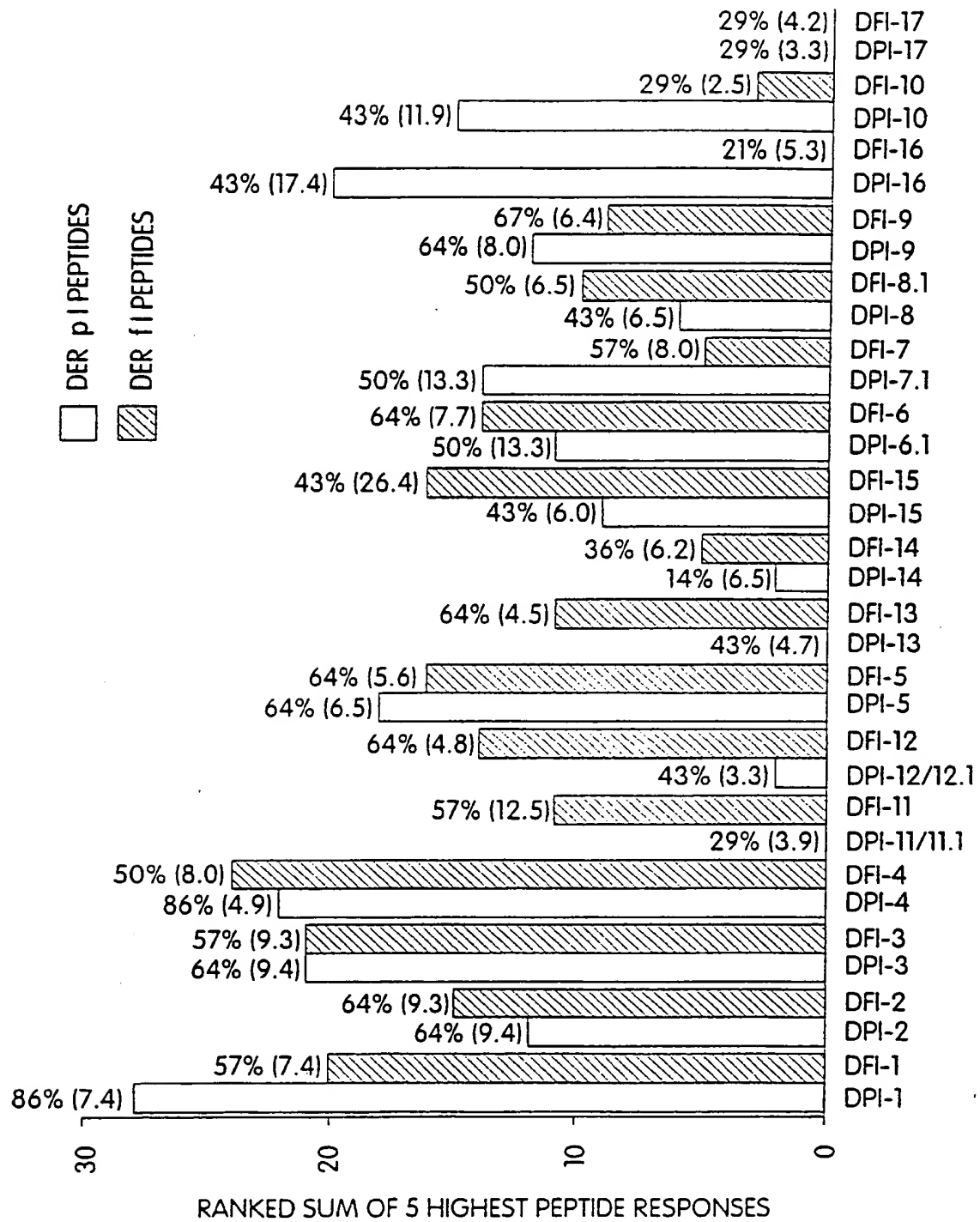


Fig. 7

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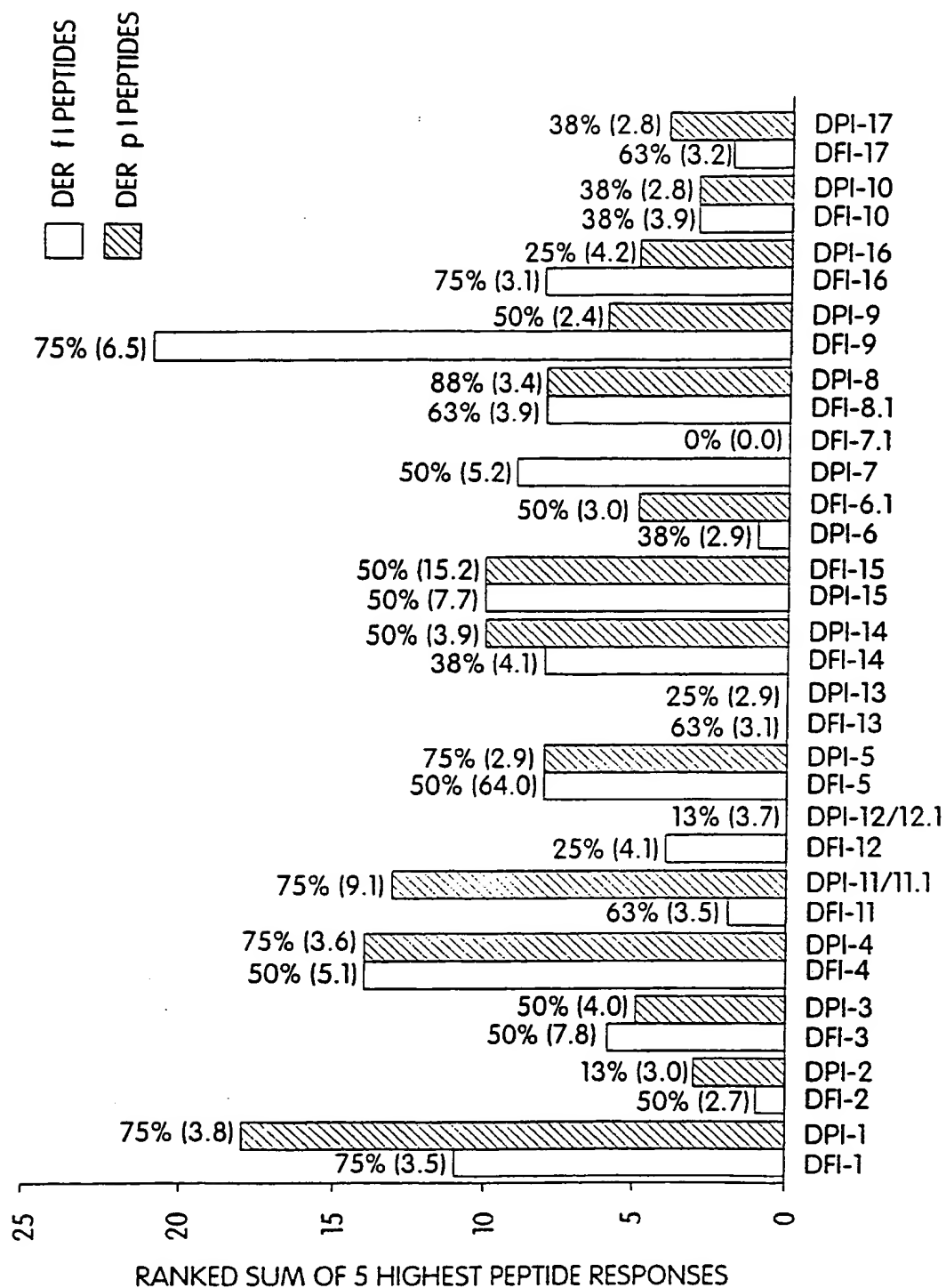


Fig. 8

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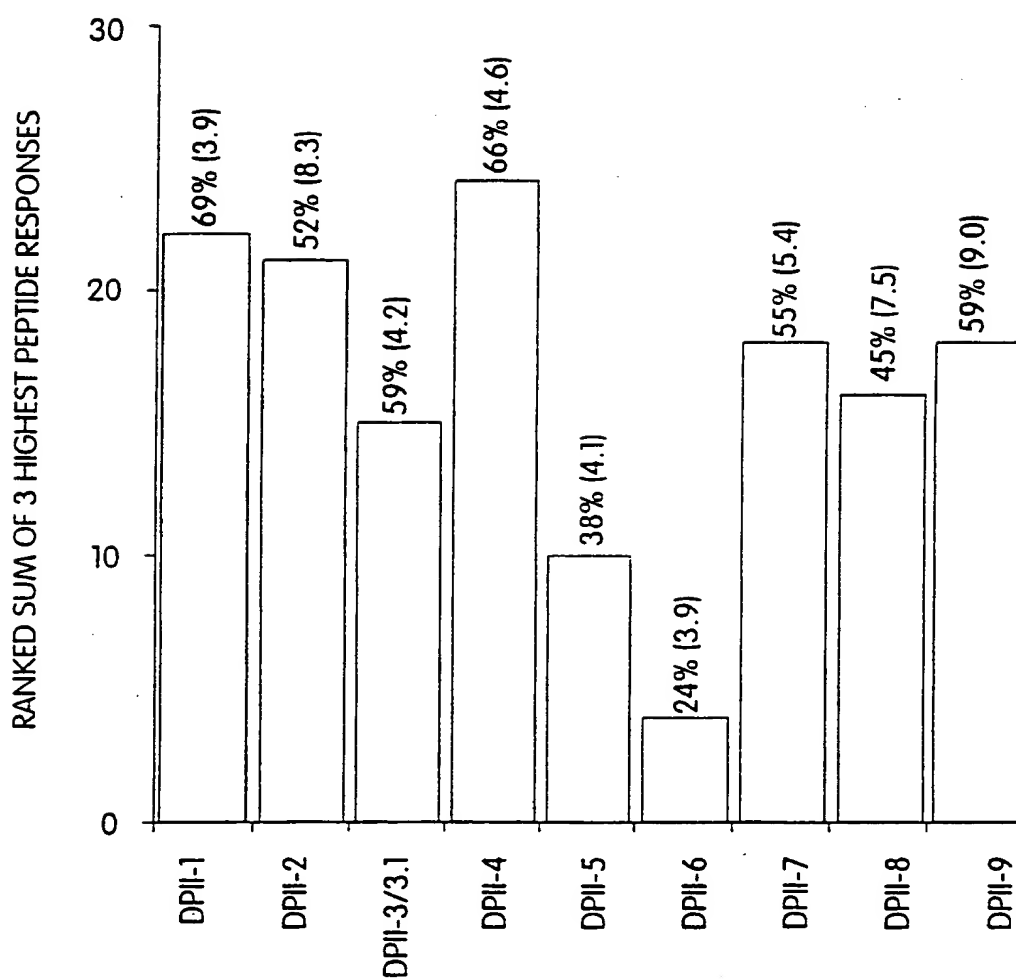


Fig. 9

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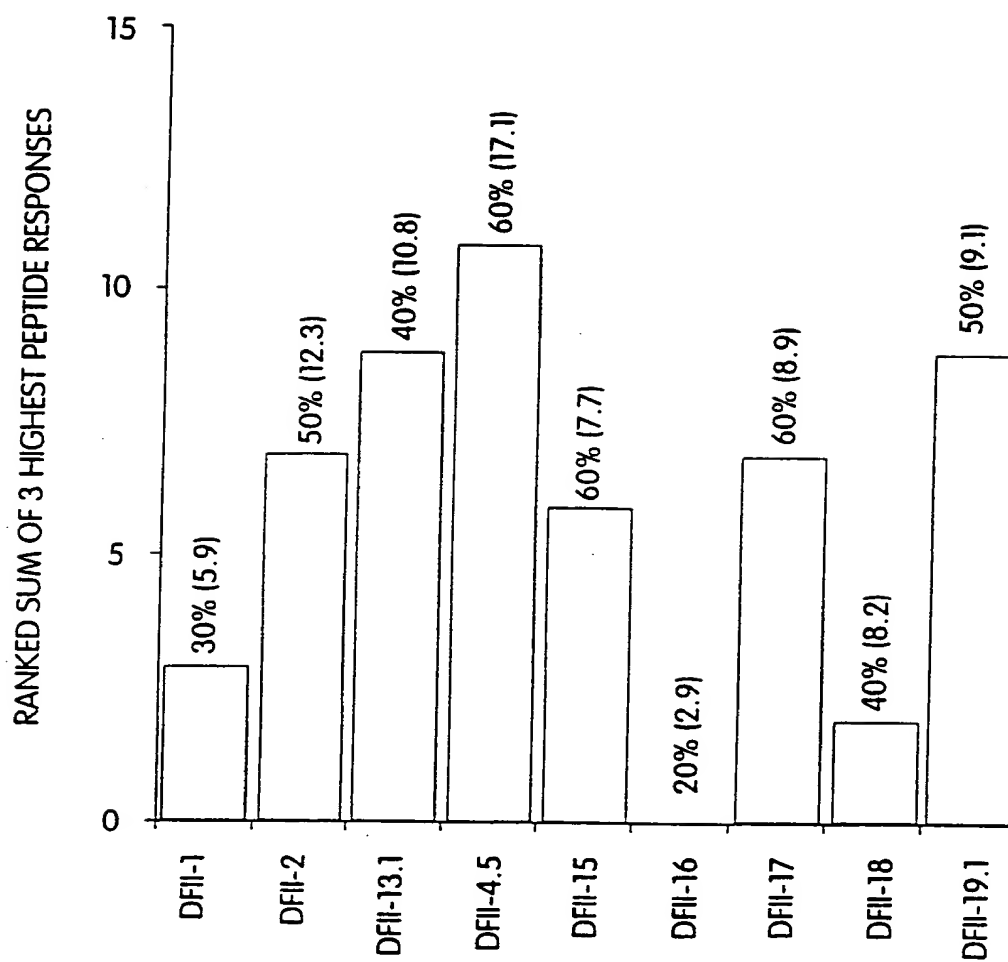


Fig. 10

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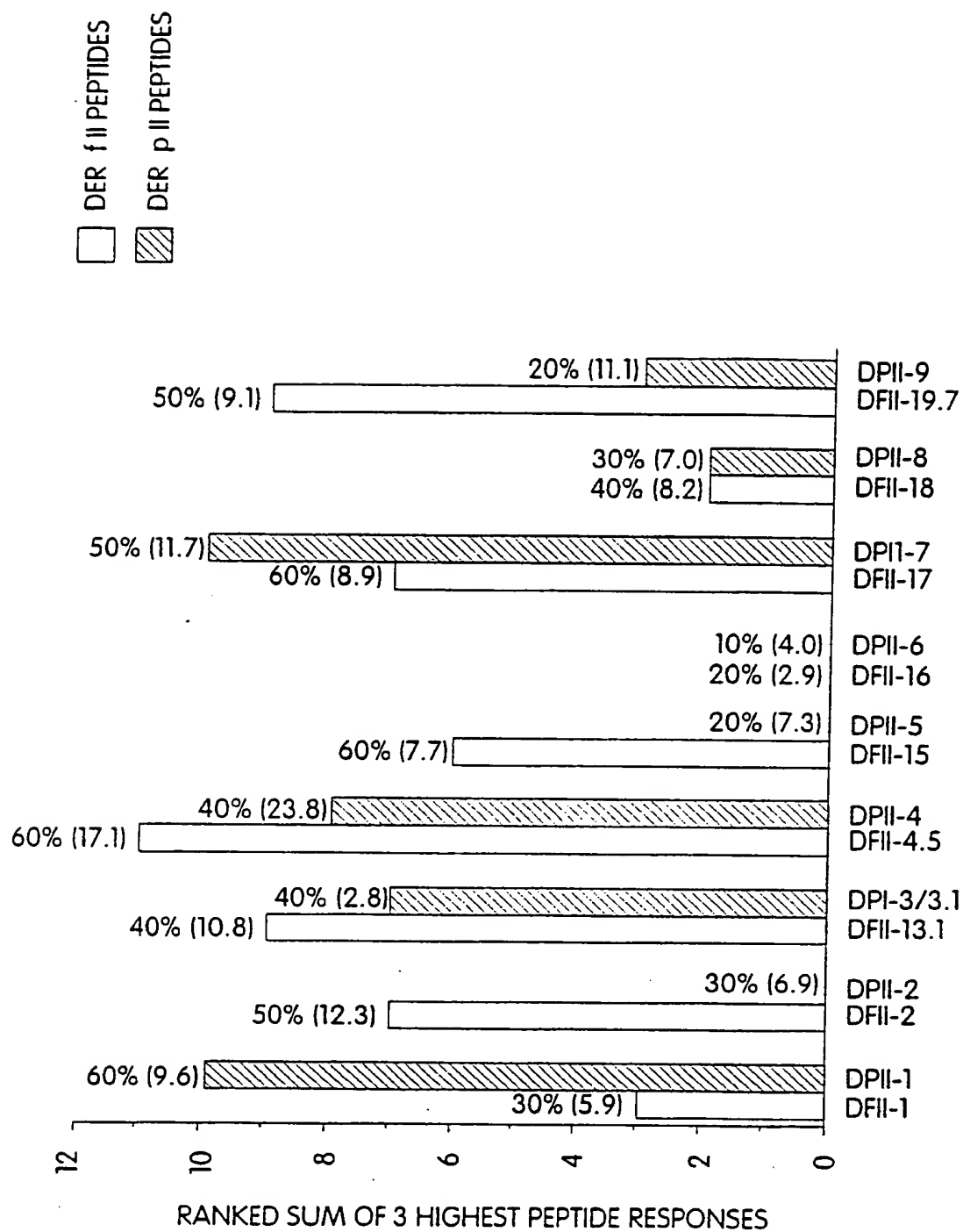


Fig. 11

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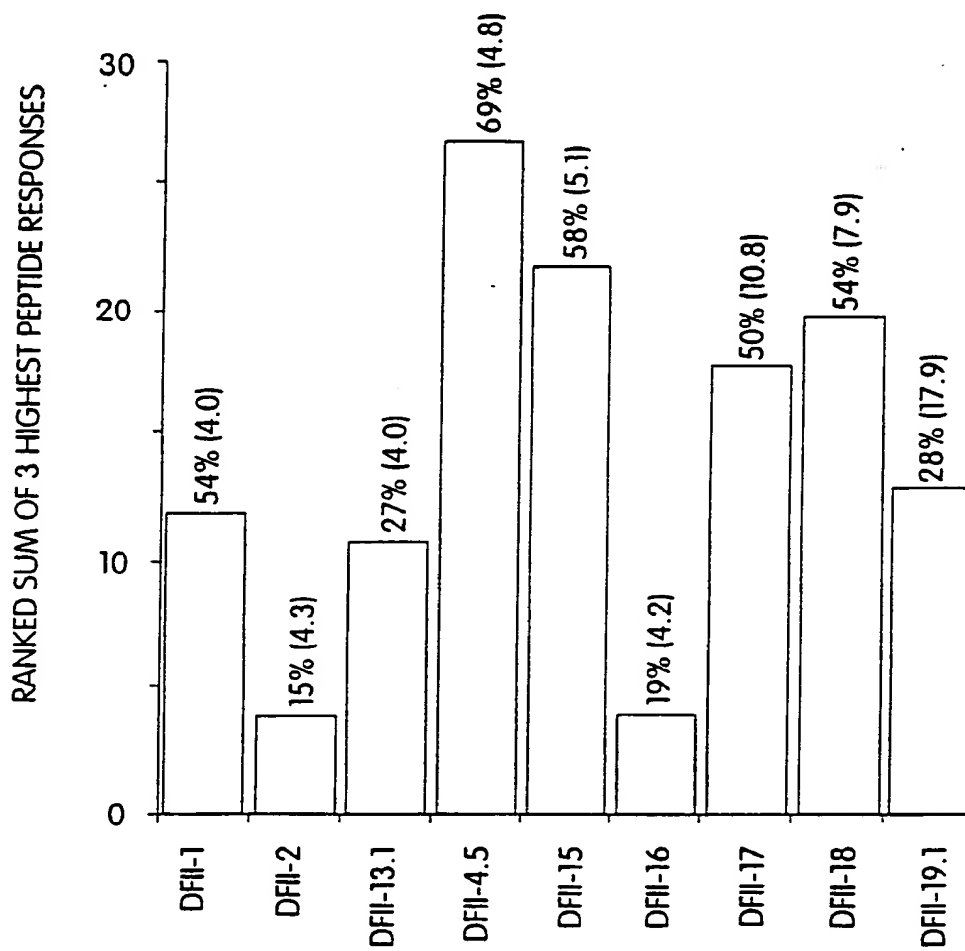


Fig. 12

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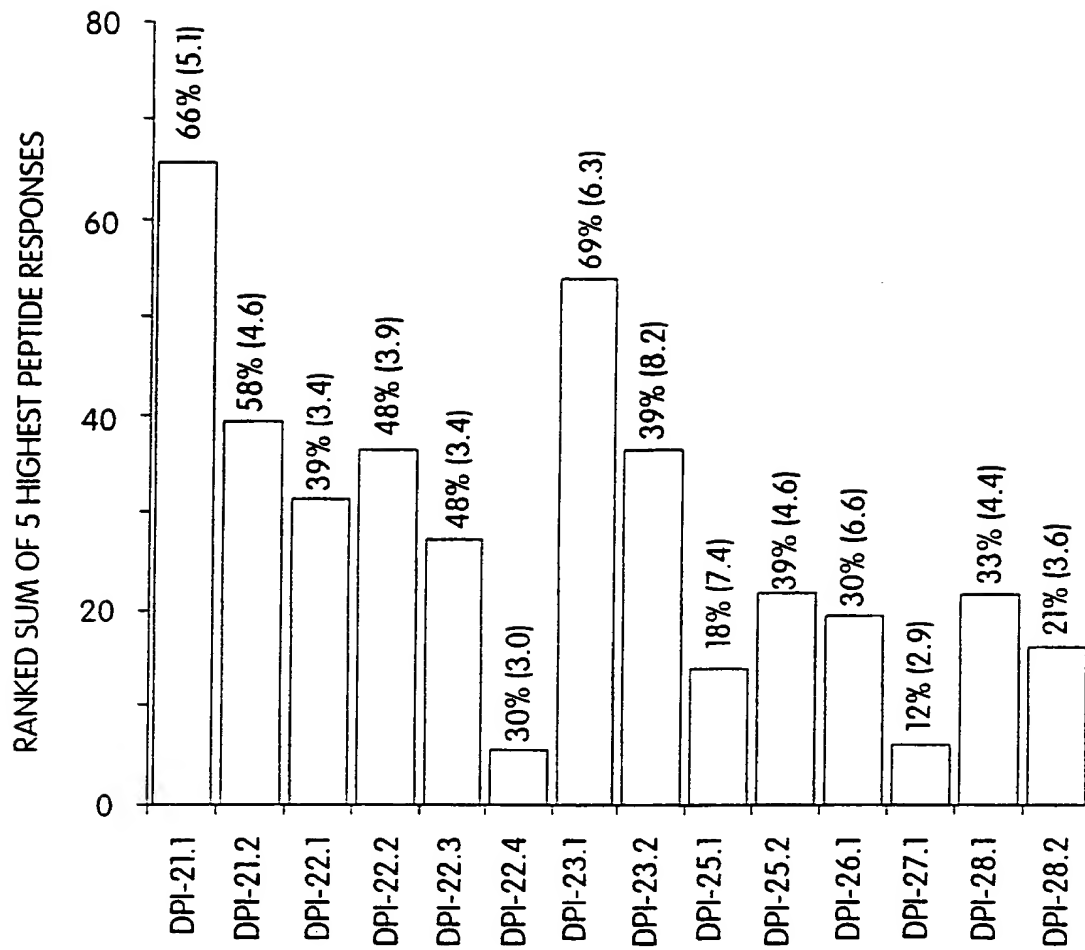


Fig. 13

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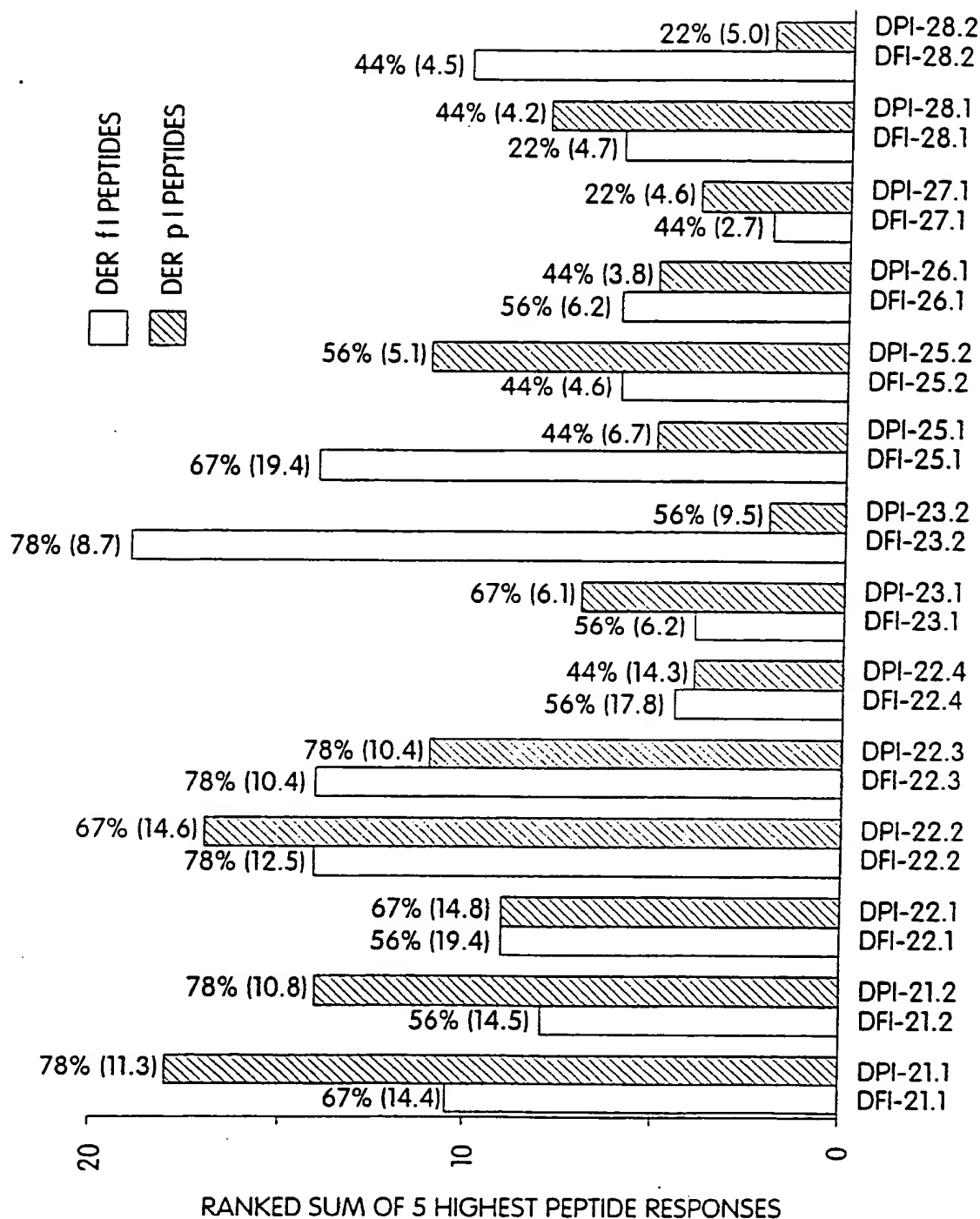


Fig. 14



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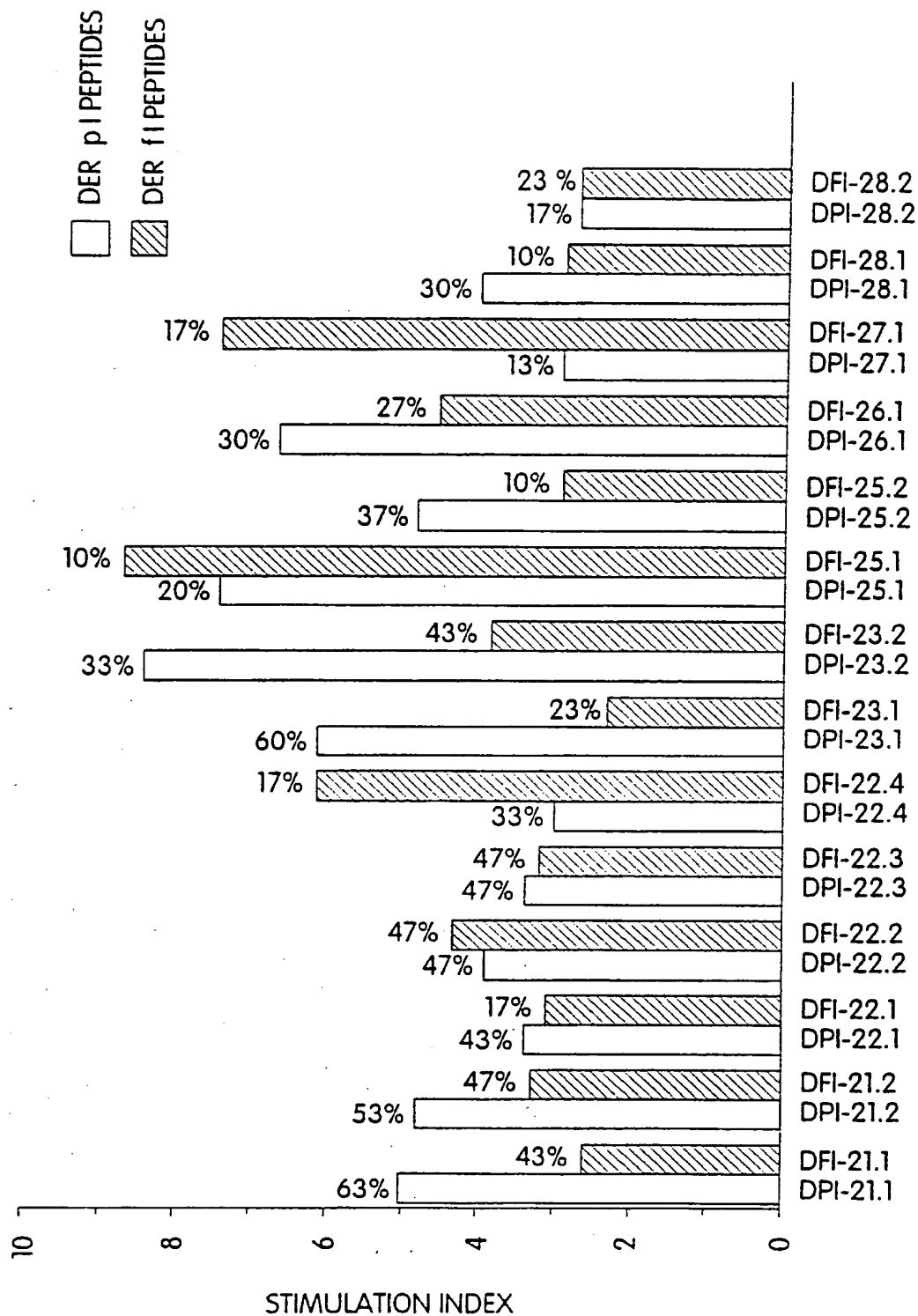


Fig. 15a

19/49

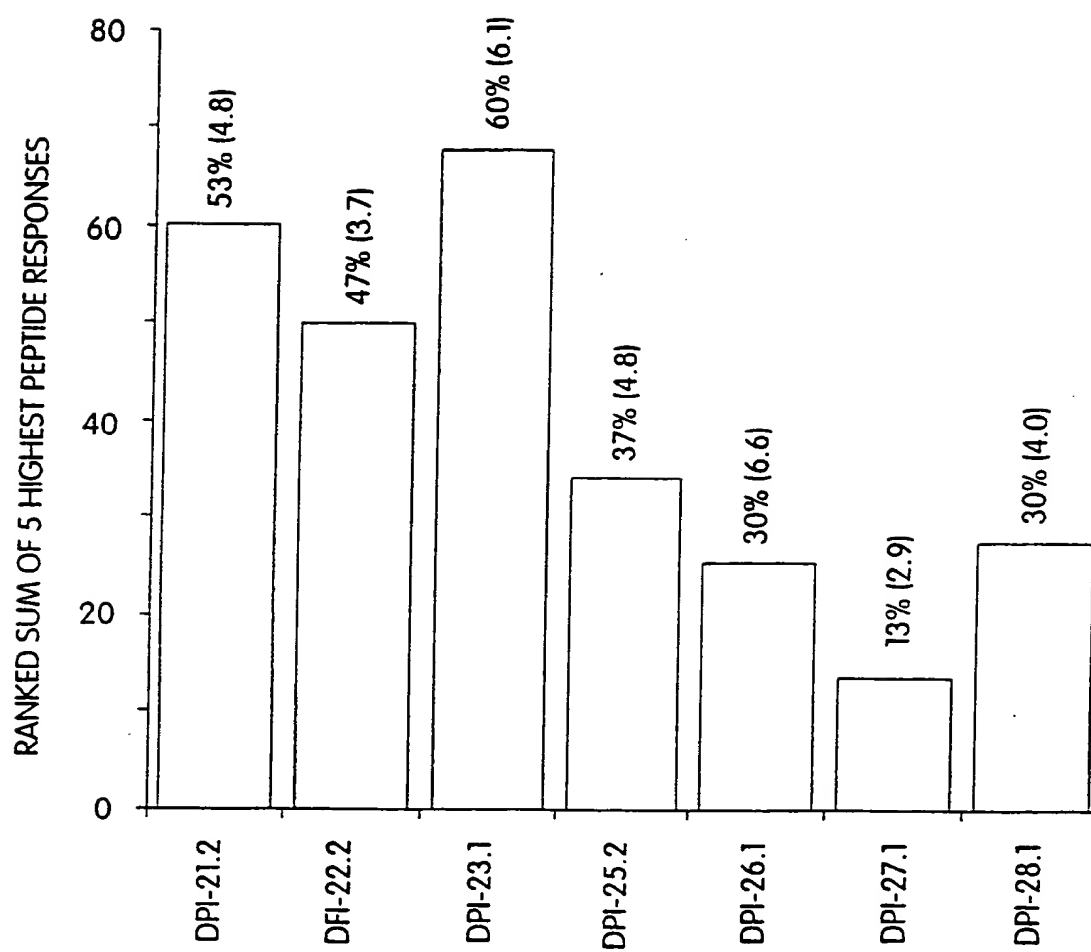


Fig. 15b

20/49

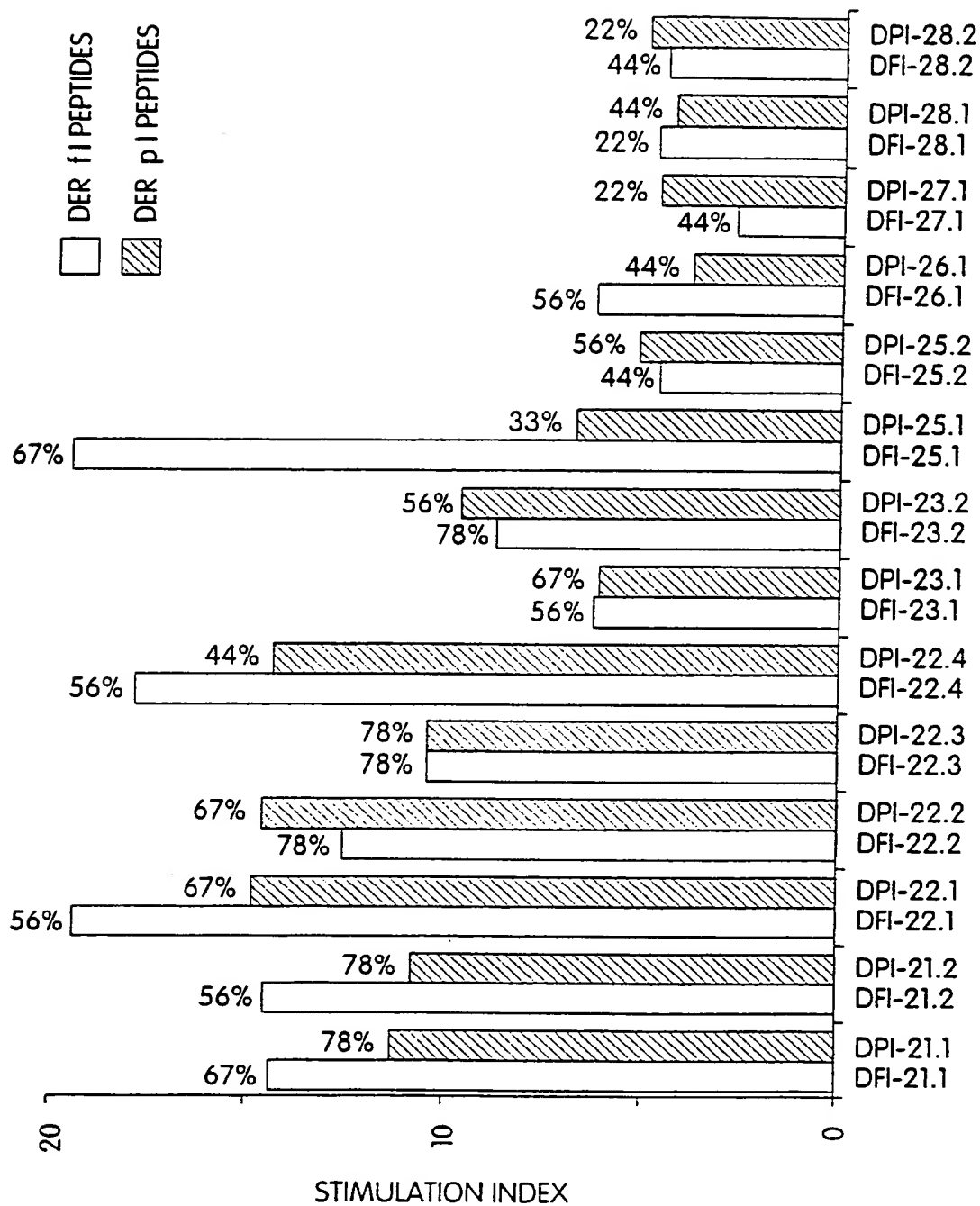


Fig. 16a

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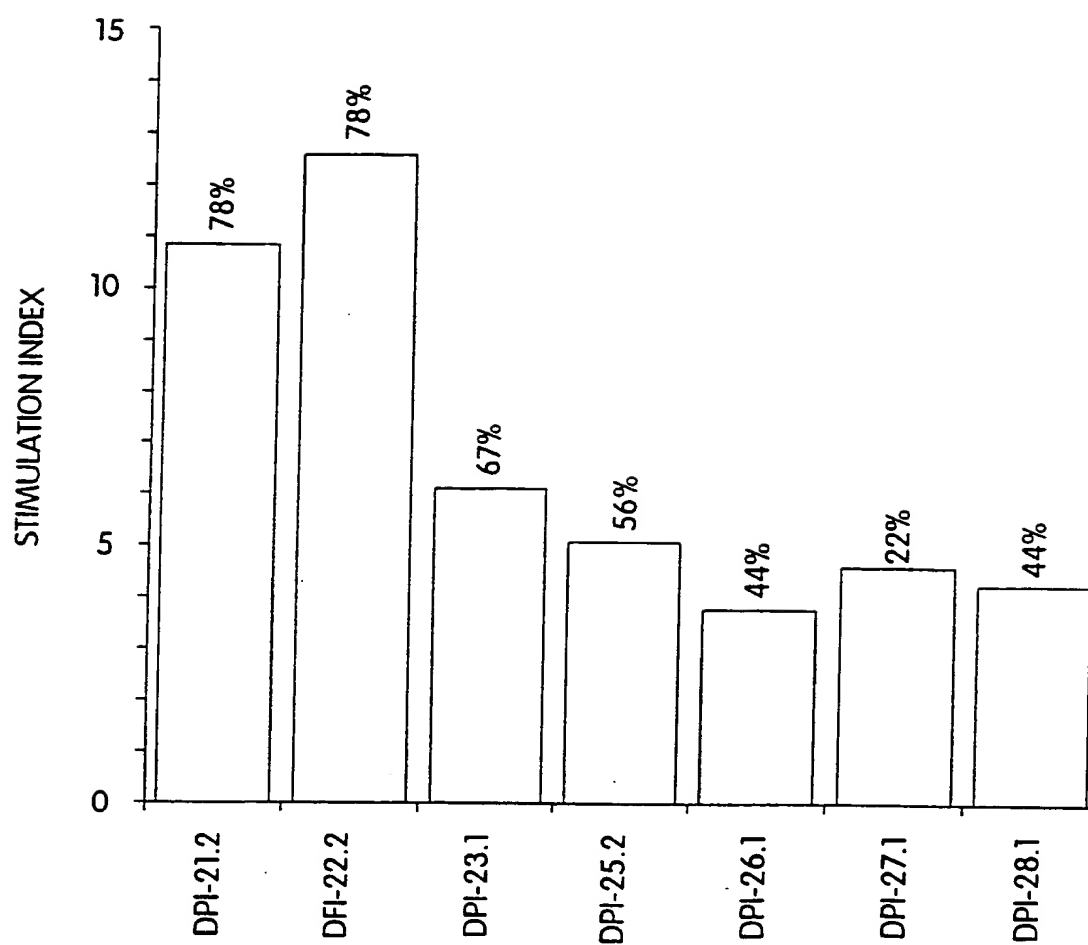


Fig. 16b

22/49

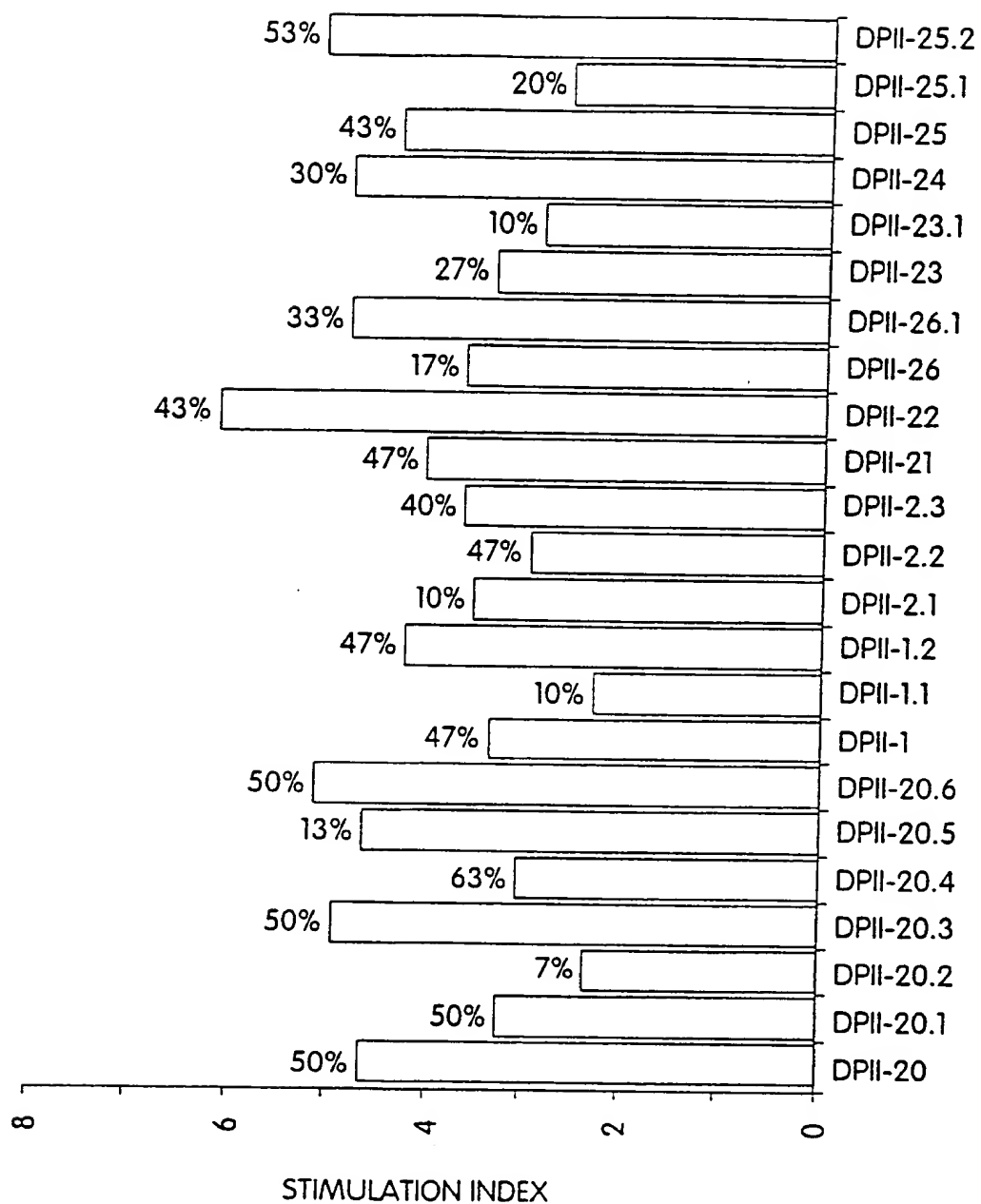


Fig. 17a

23/49

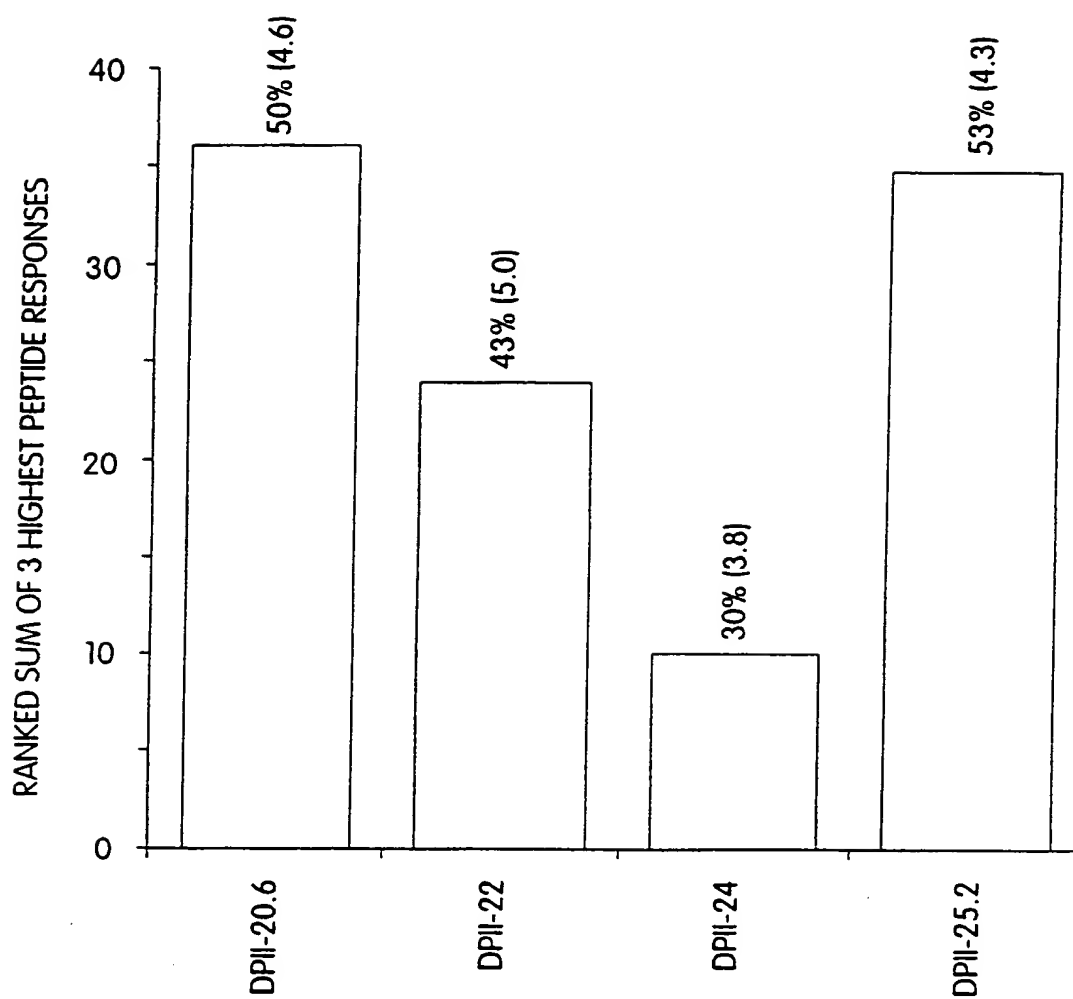


Fig. 17b

24/49

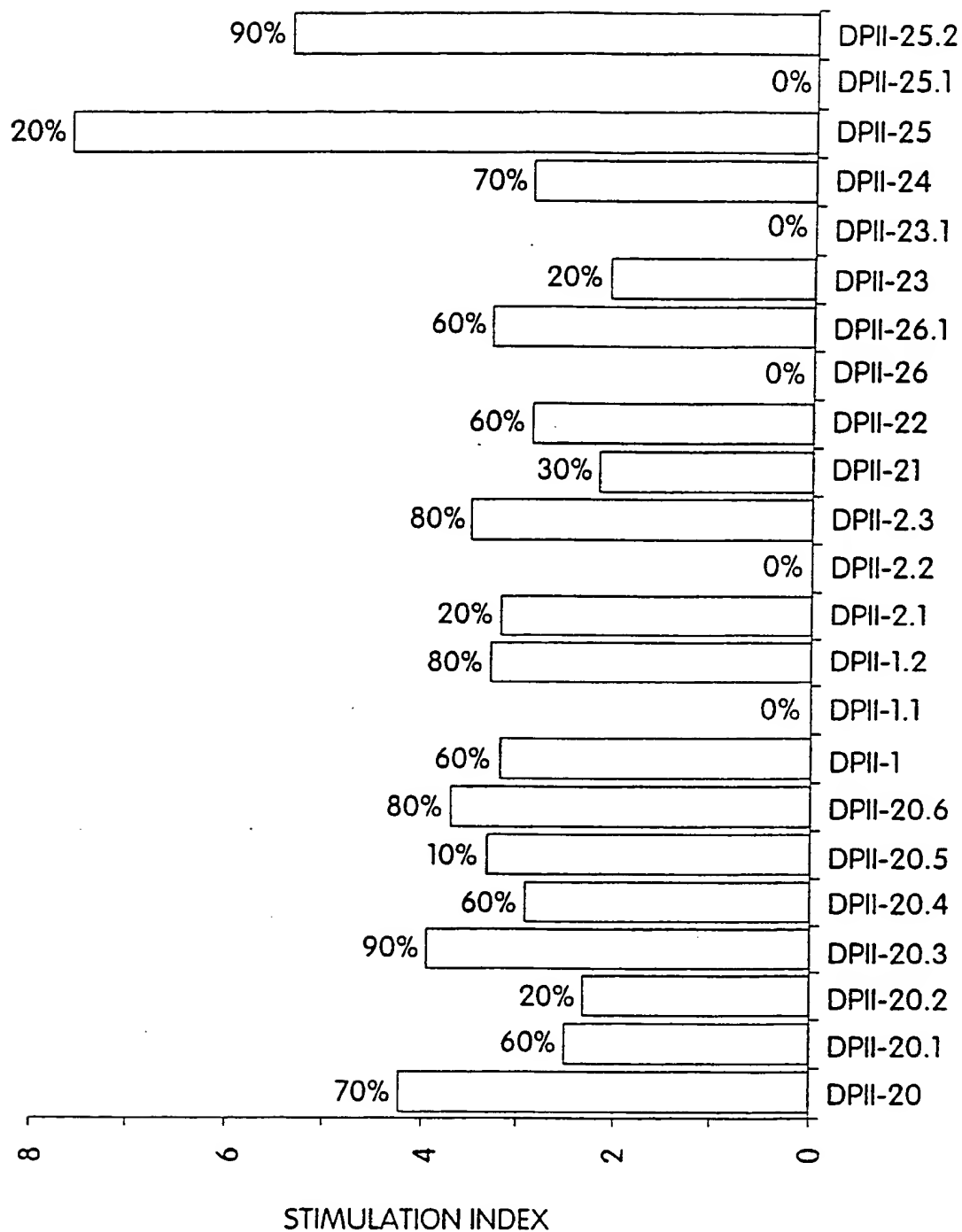


Fig. 18a

25/49

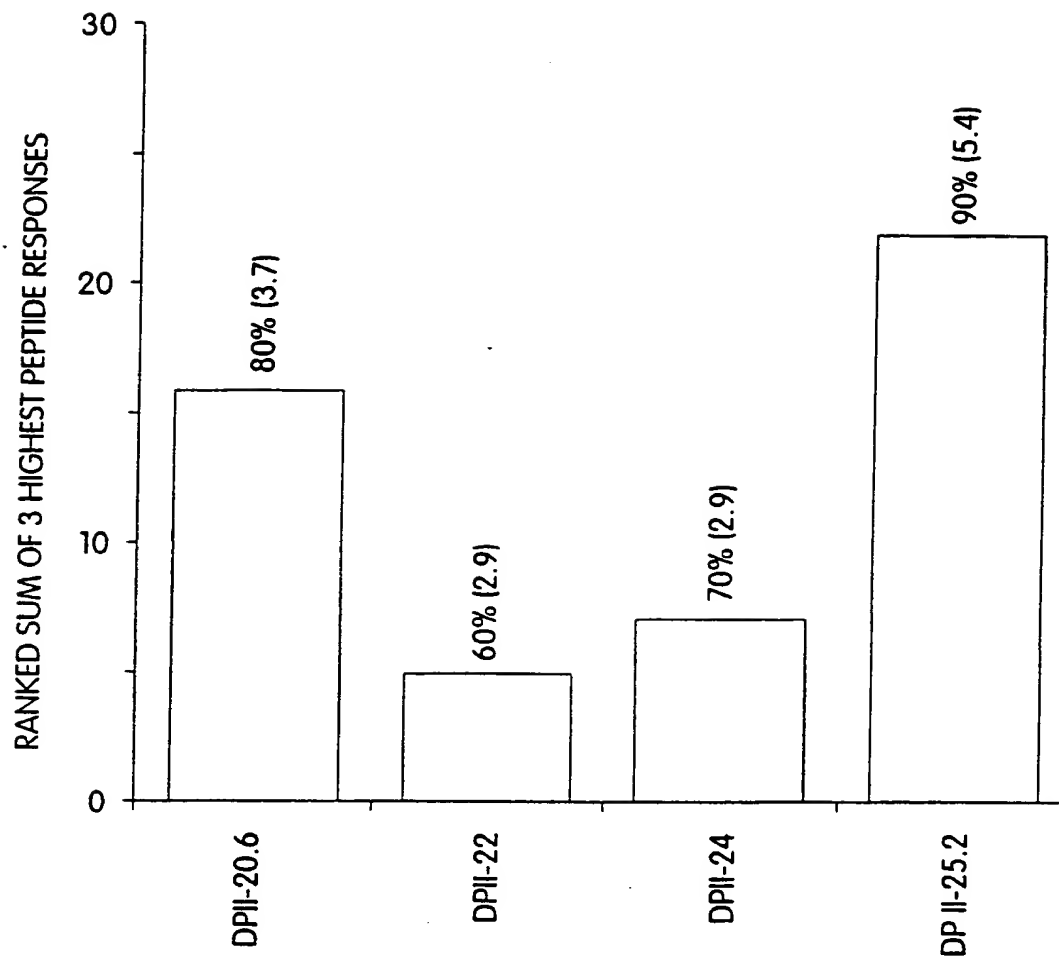


Fig. 18b



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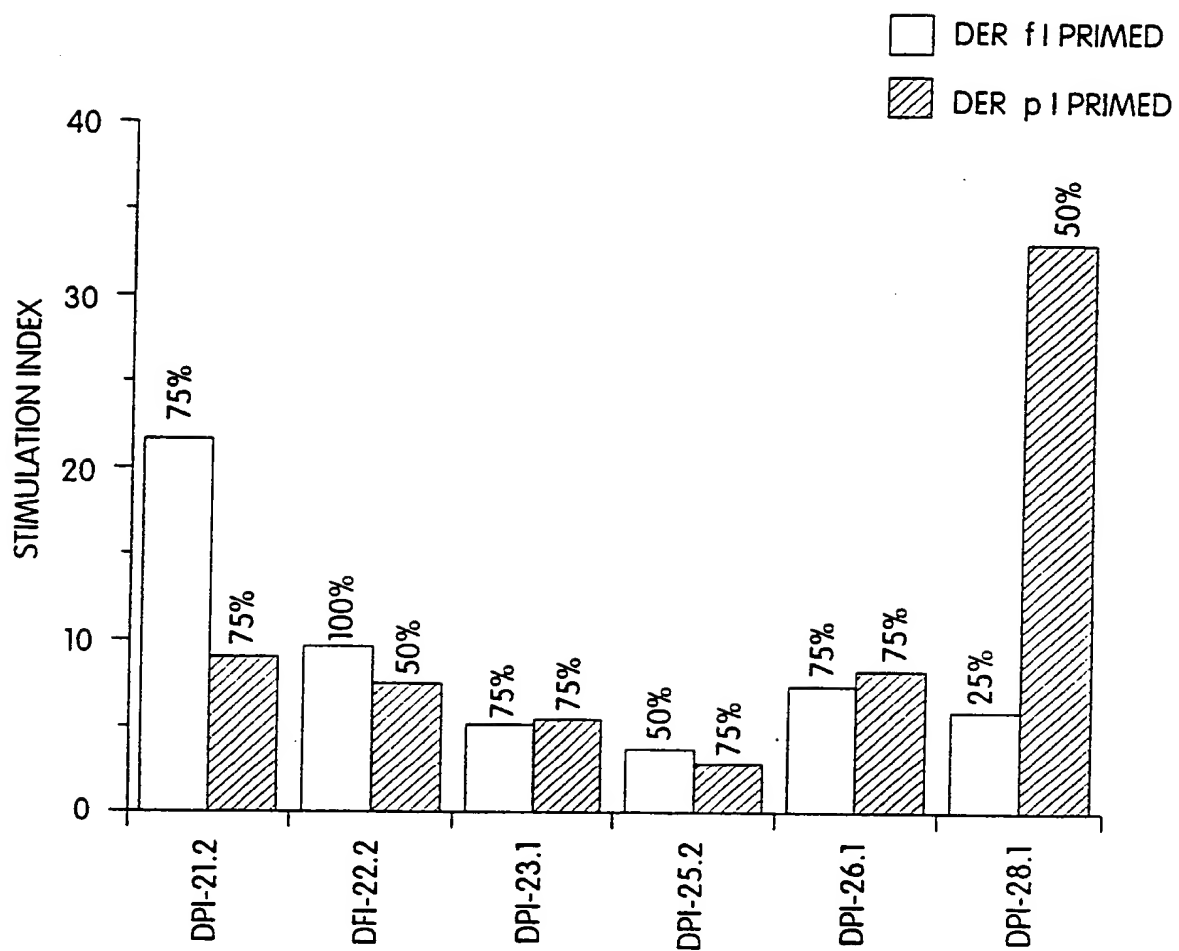


Fig. 18c

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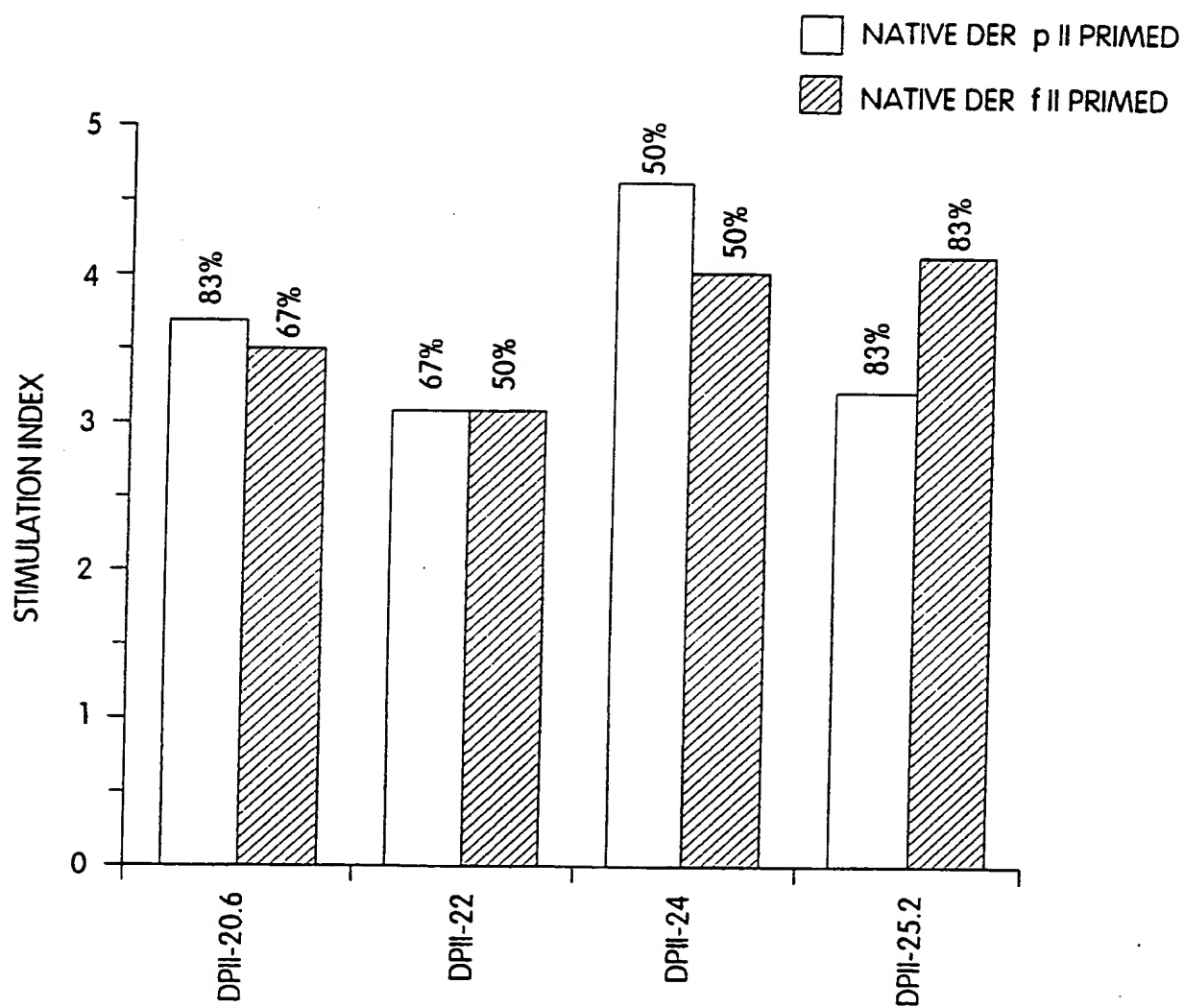


Fig. 18d

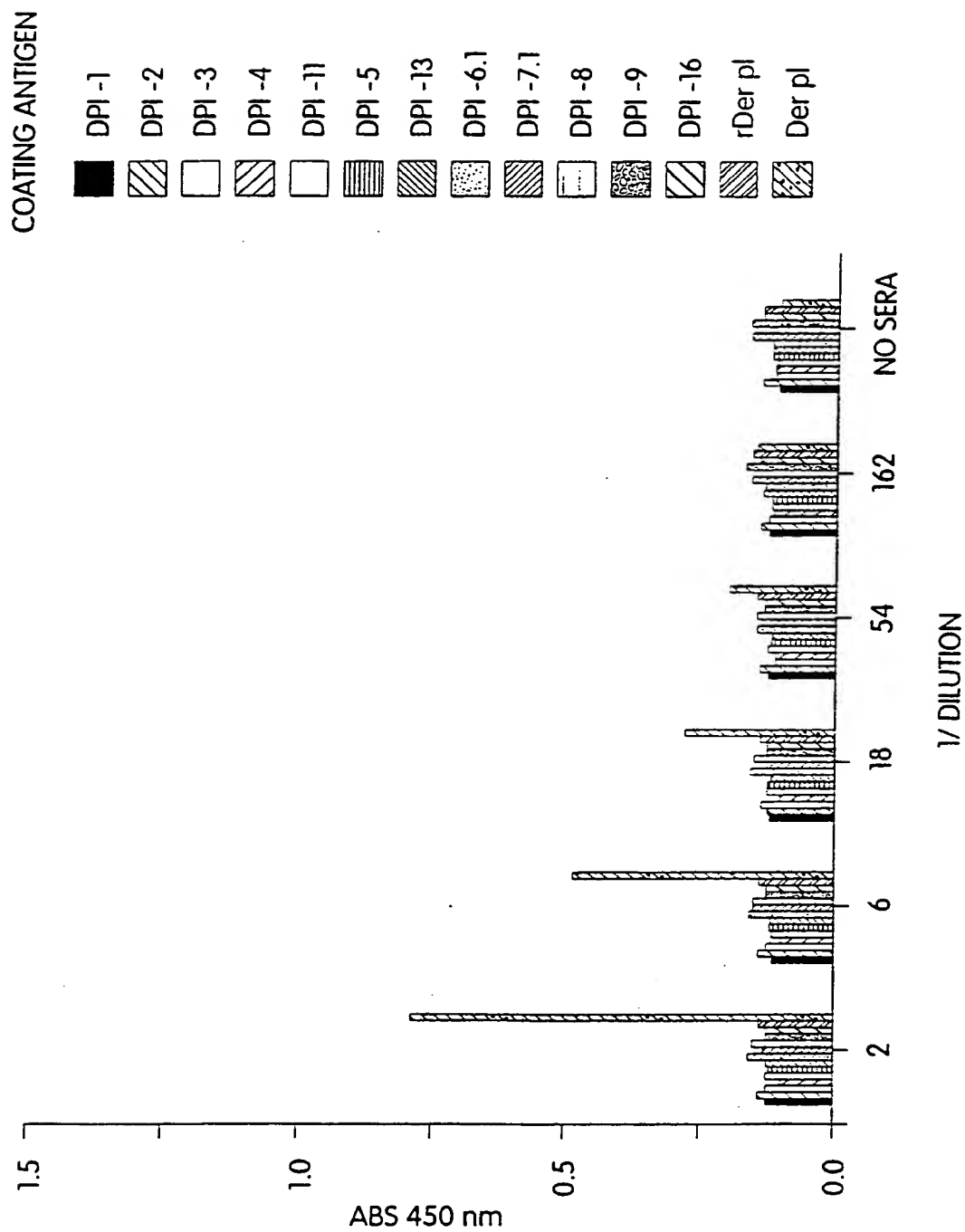


Fig. 19a

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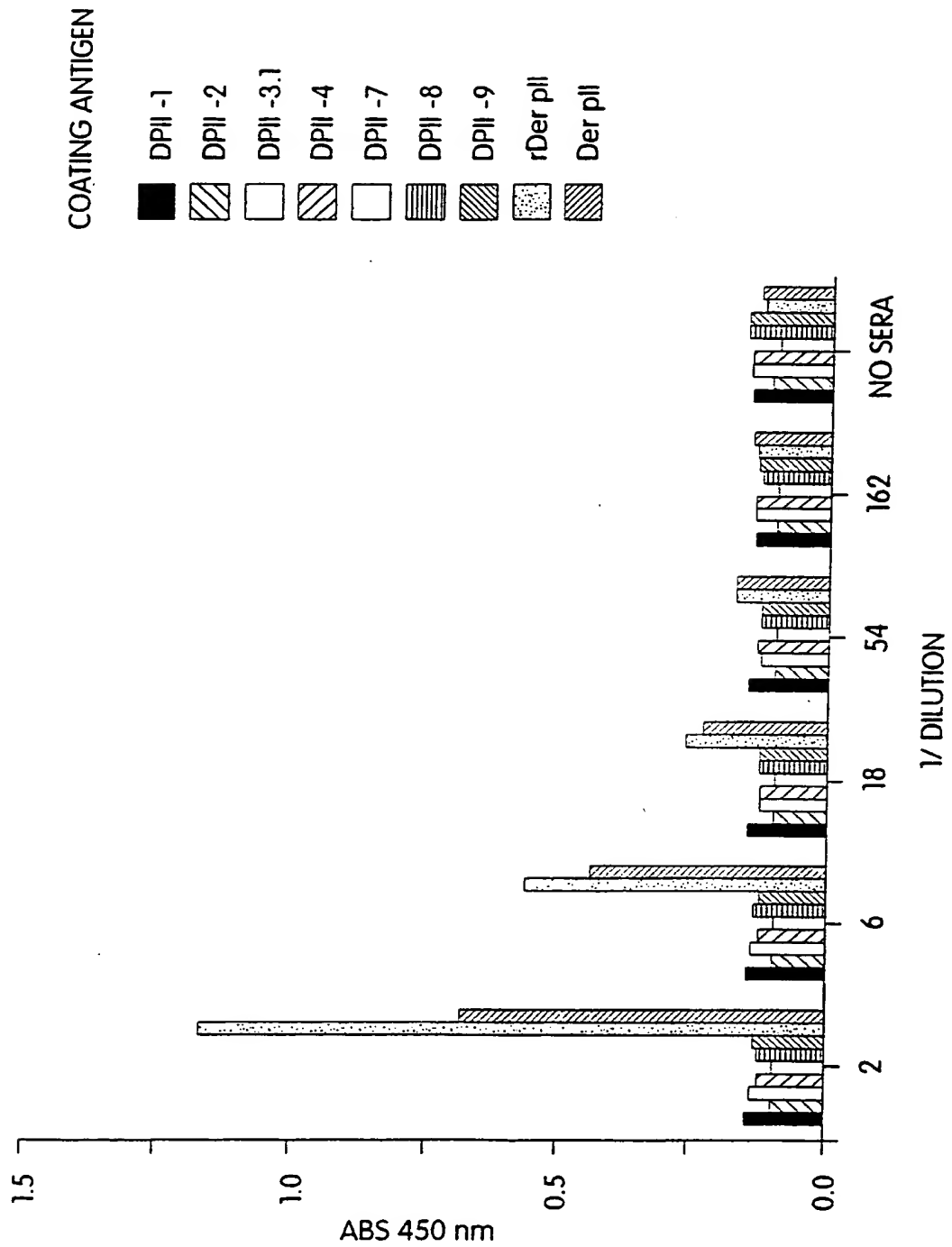


Fig. 19b

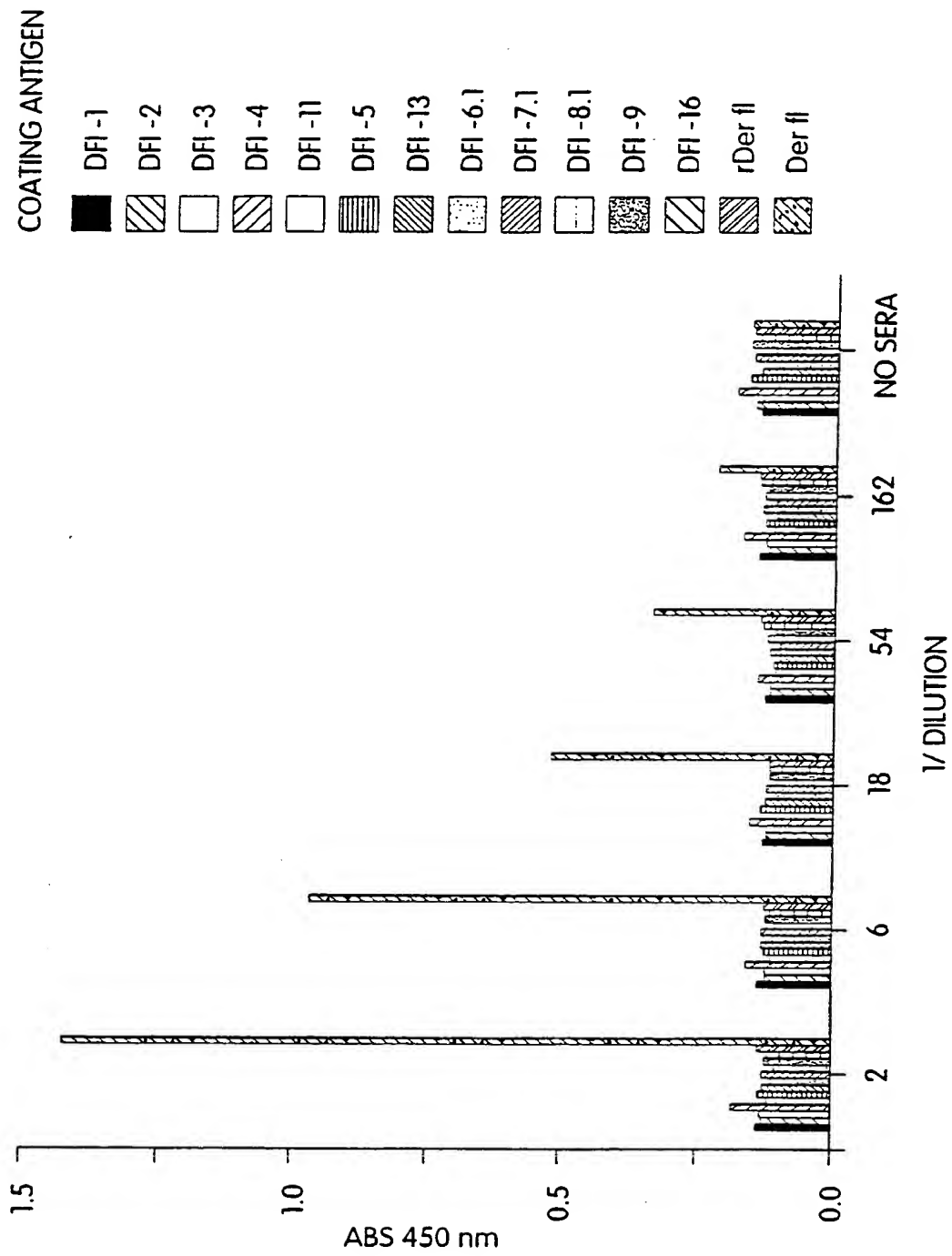


Fig. 20a

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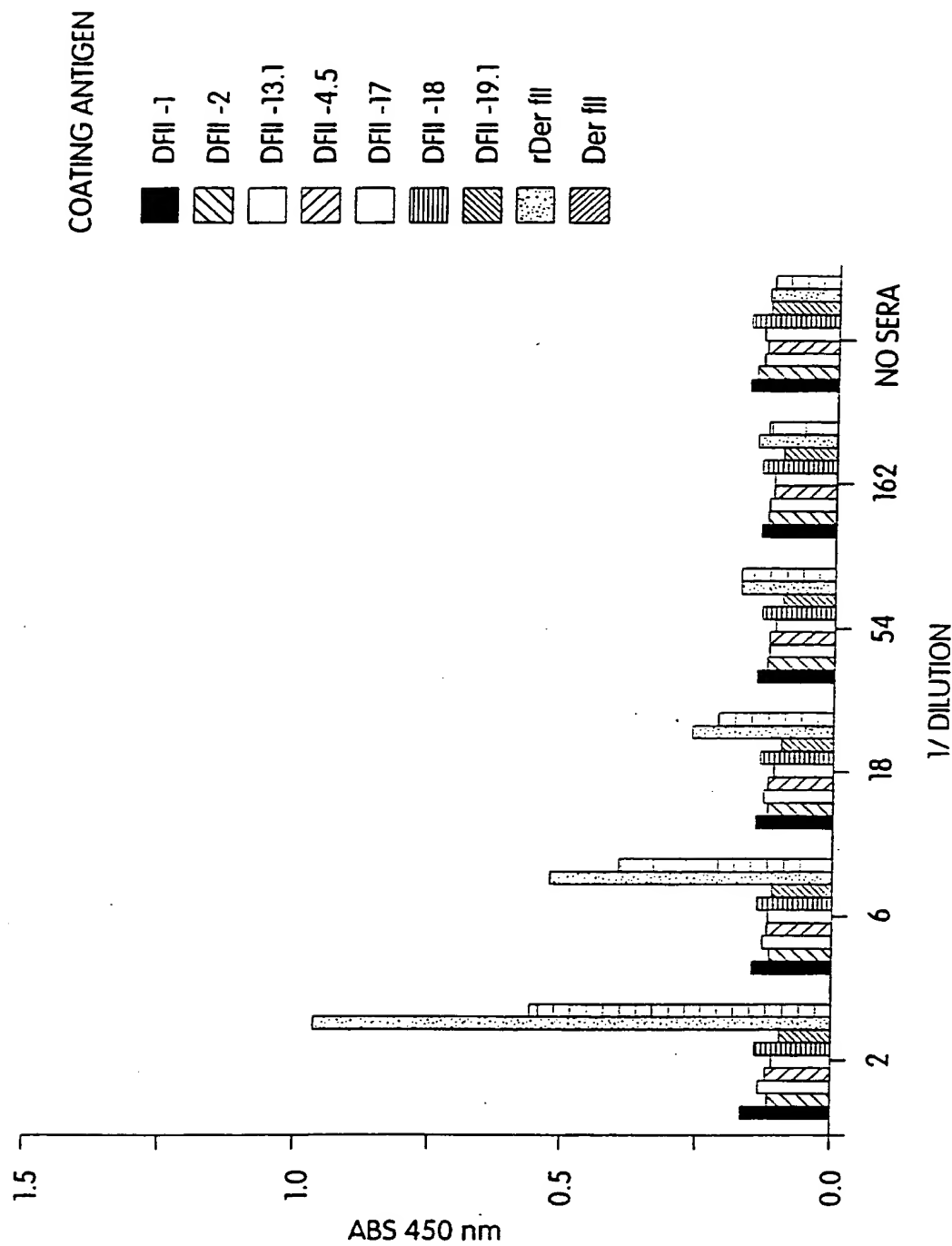


Fig. 20b

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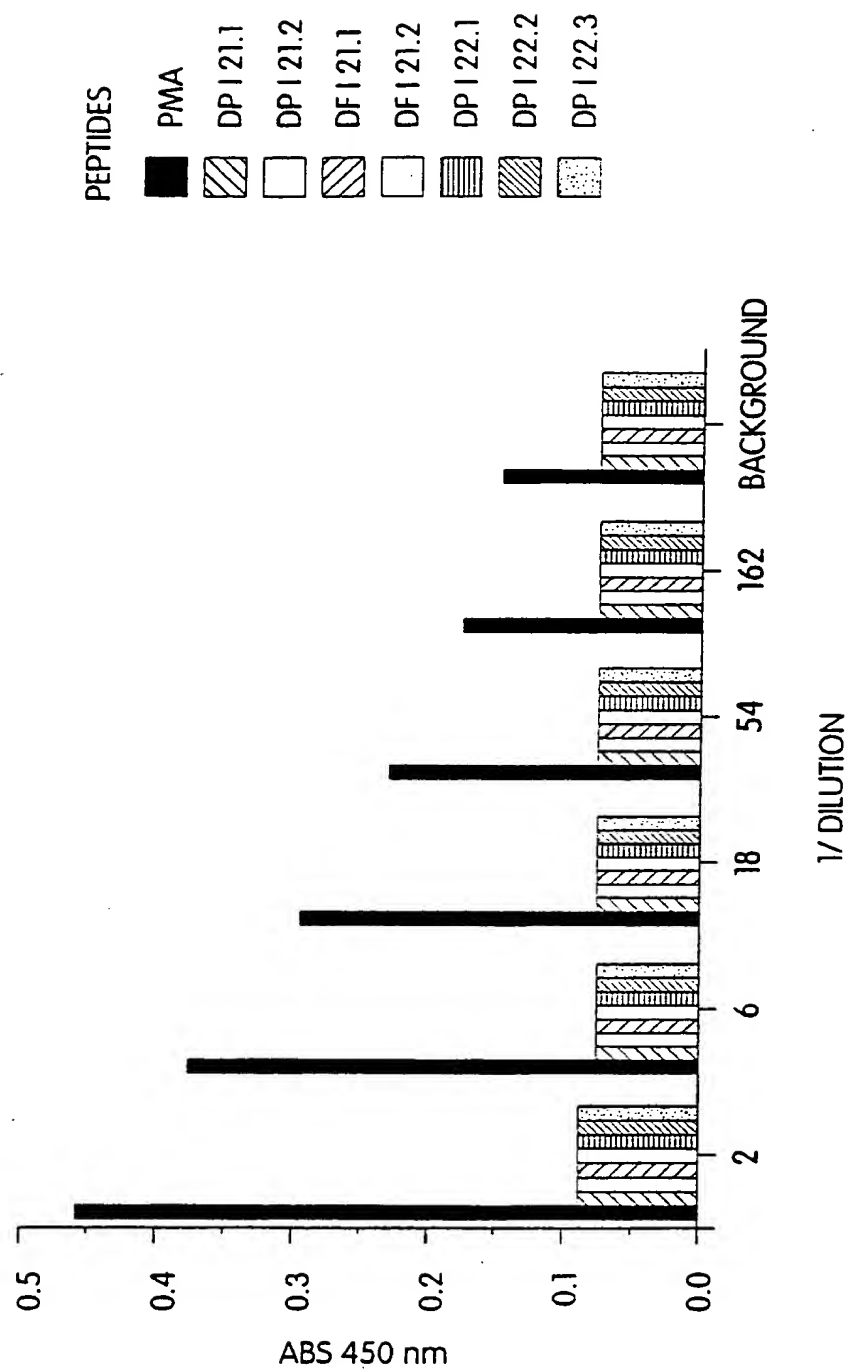


Fig. 21a

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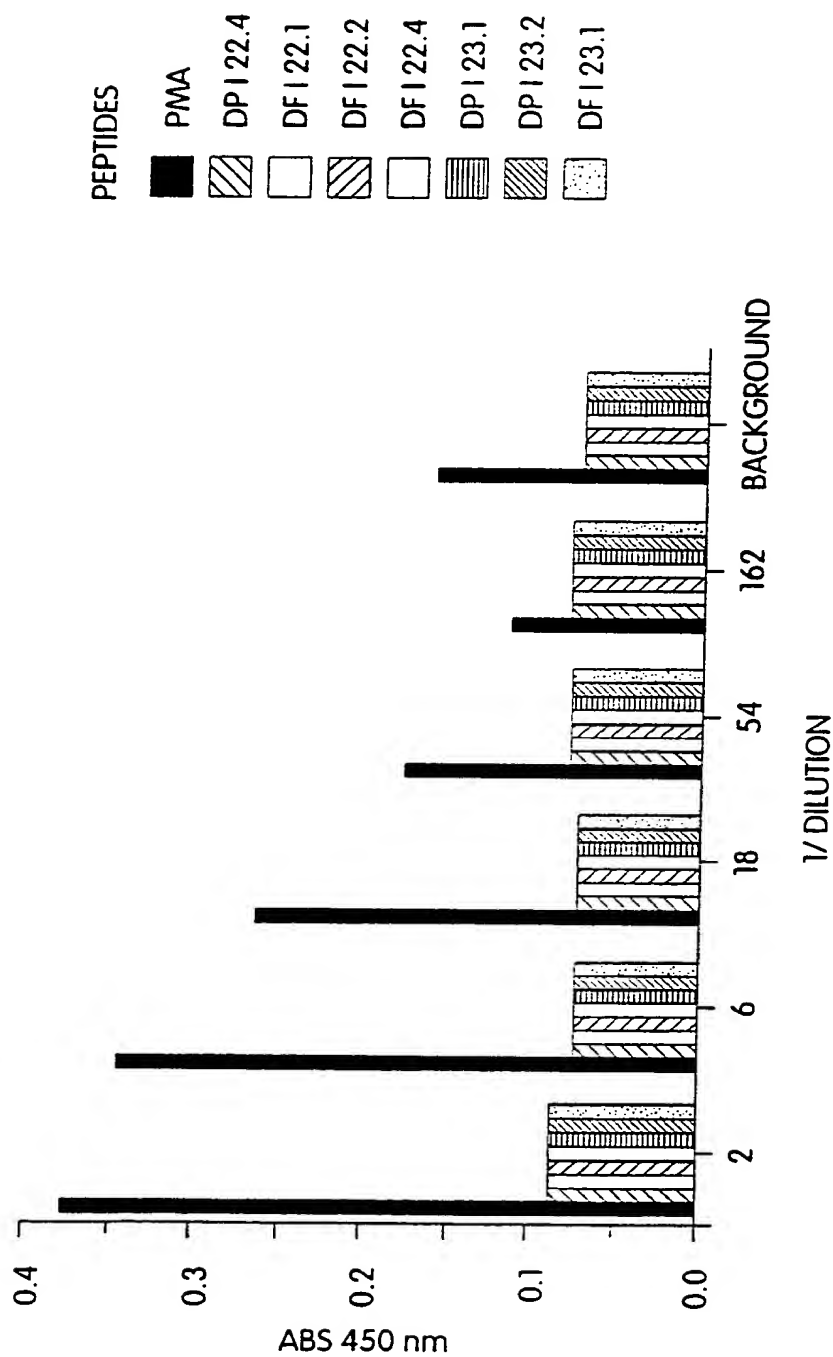


Fig. 21b



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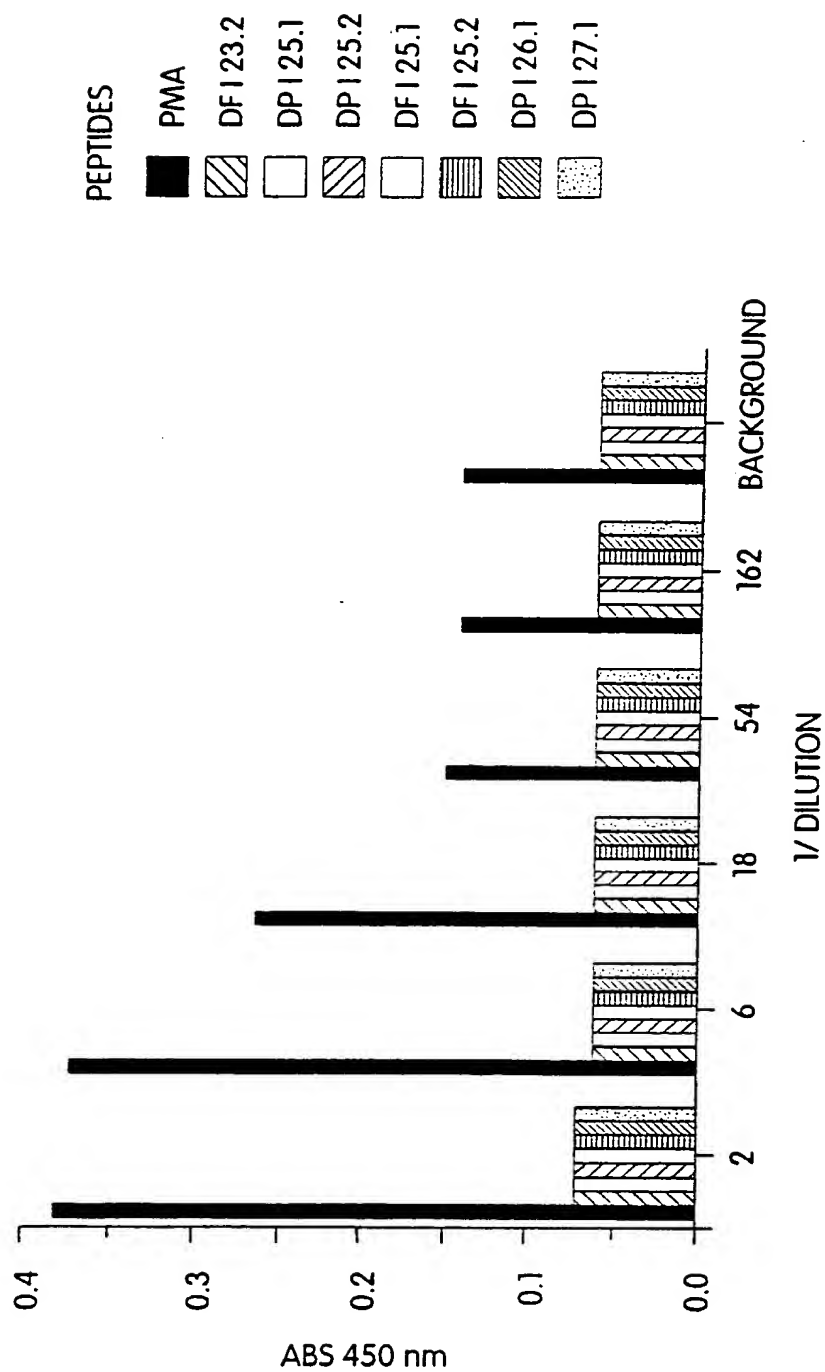


Fig. 21c

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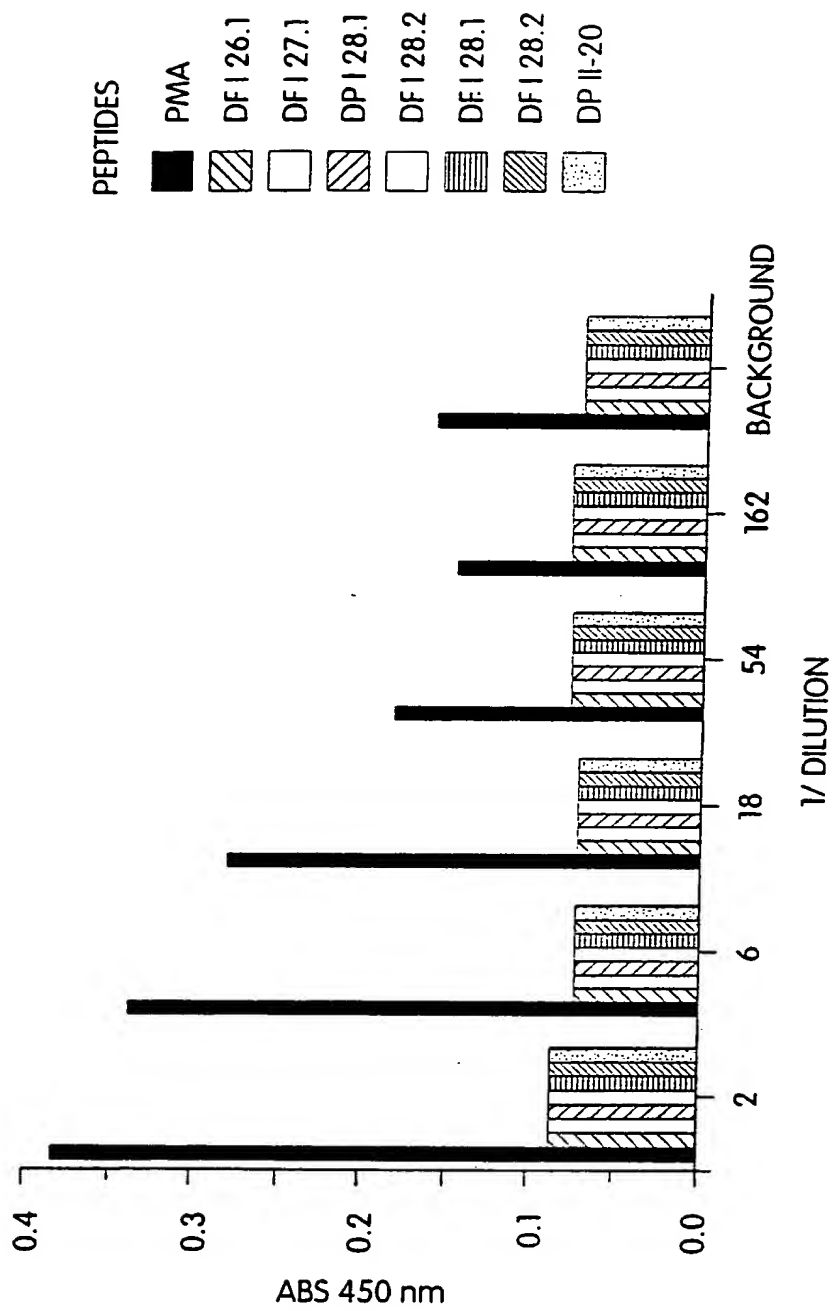


Fig. 21d

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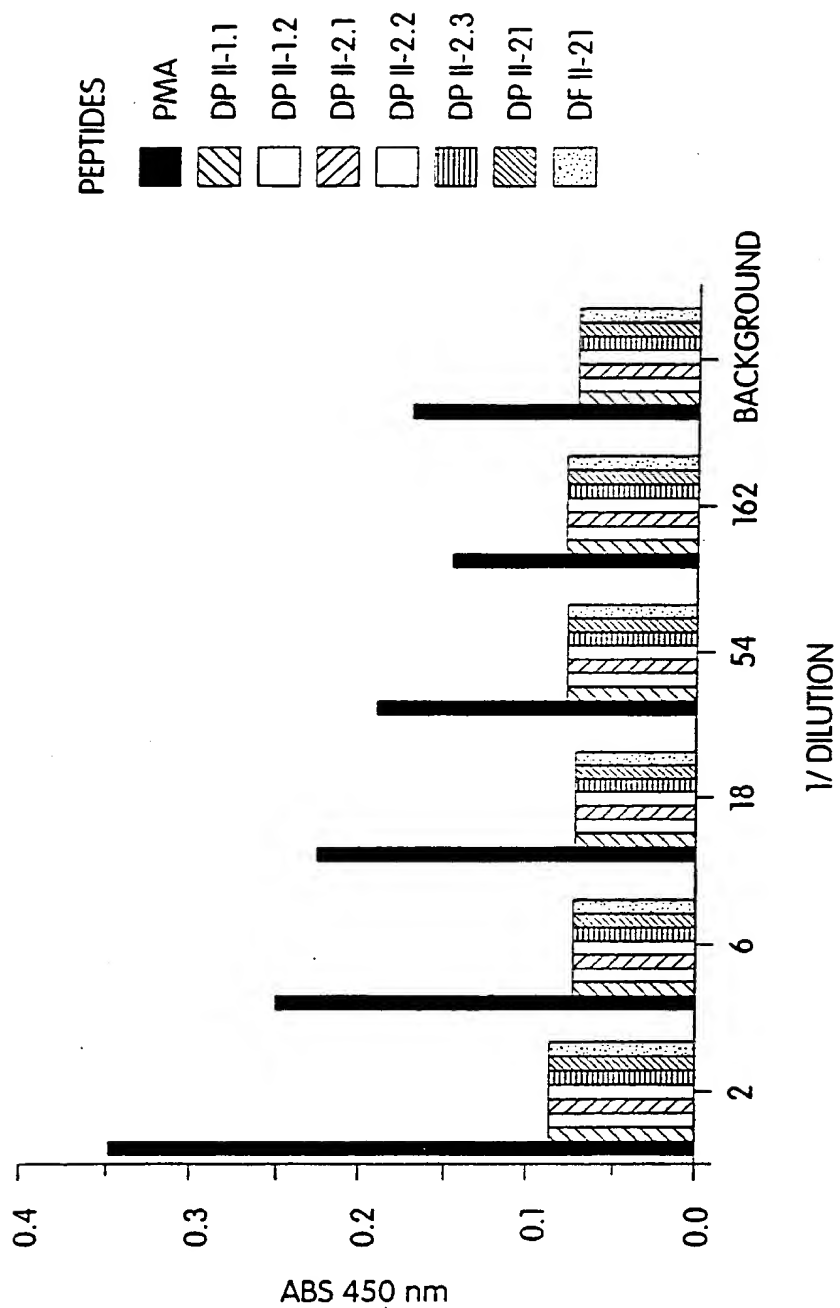


Fig. 21e

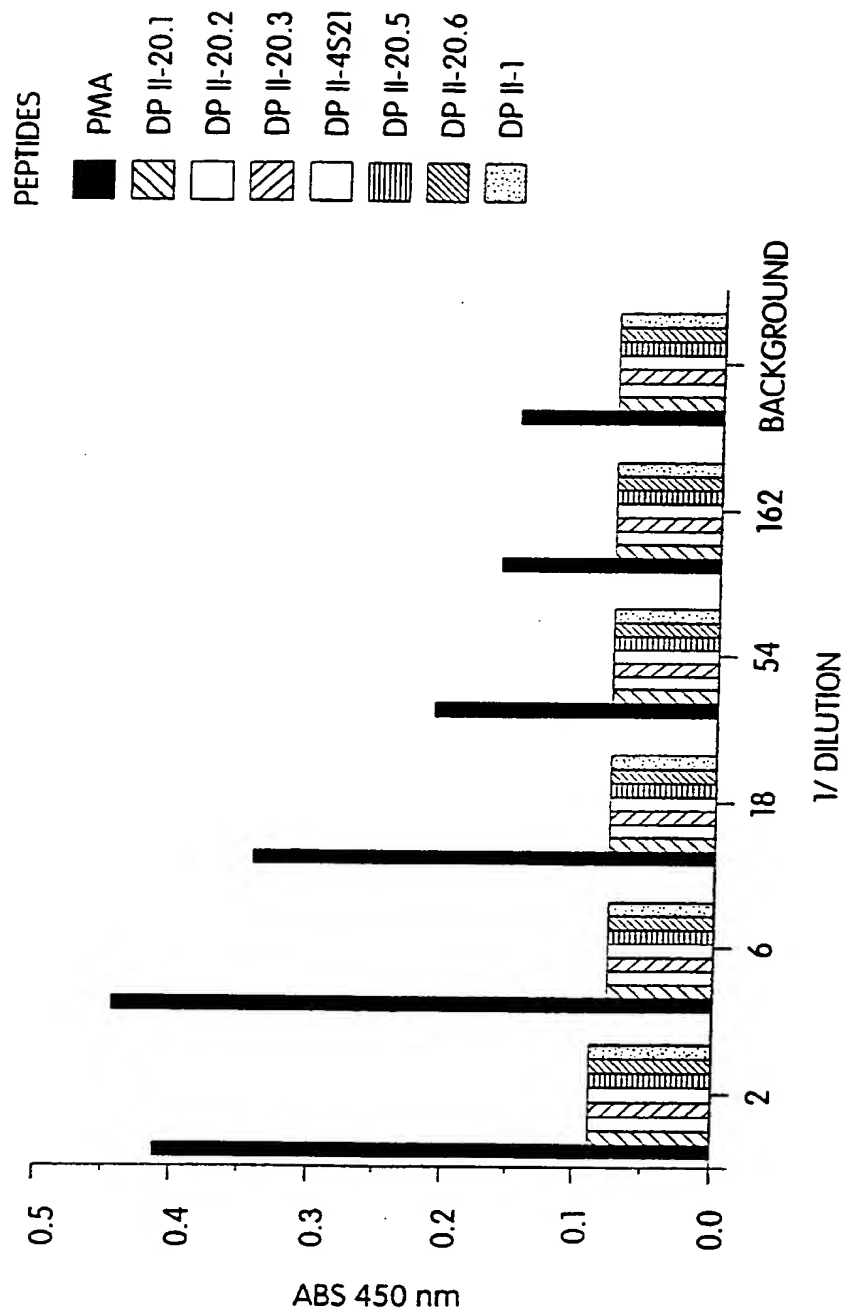


Fig. 21f

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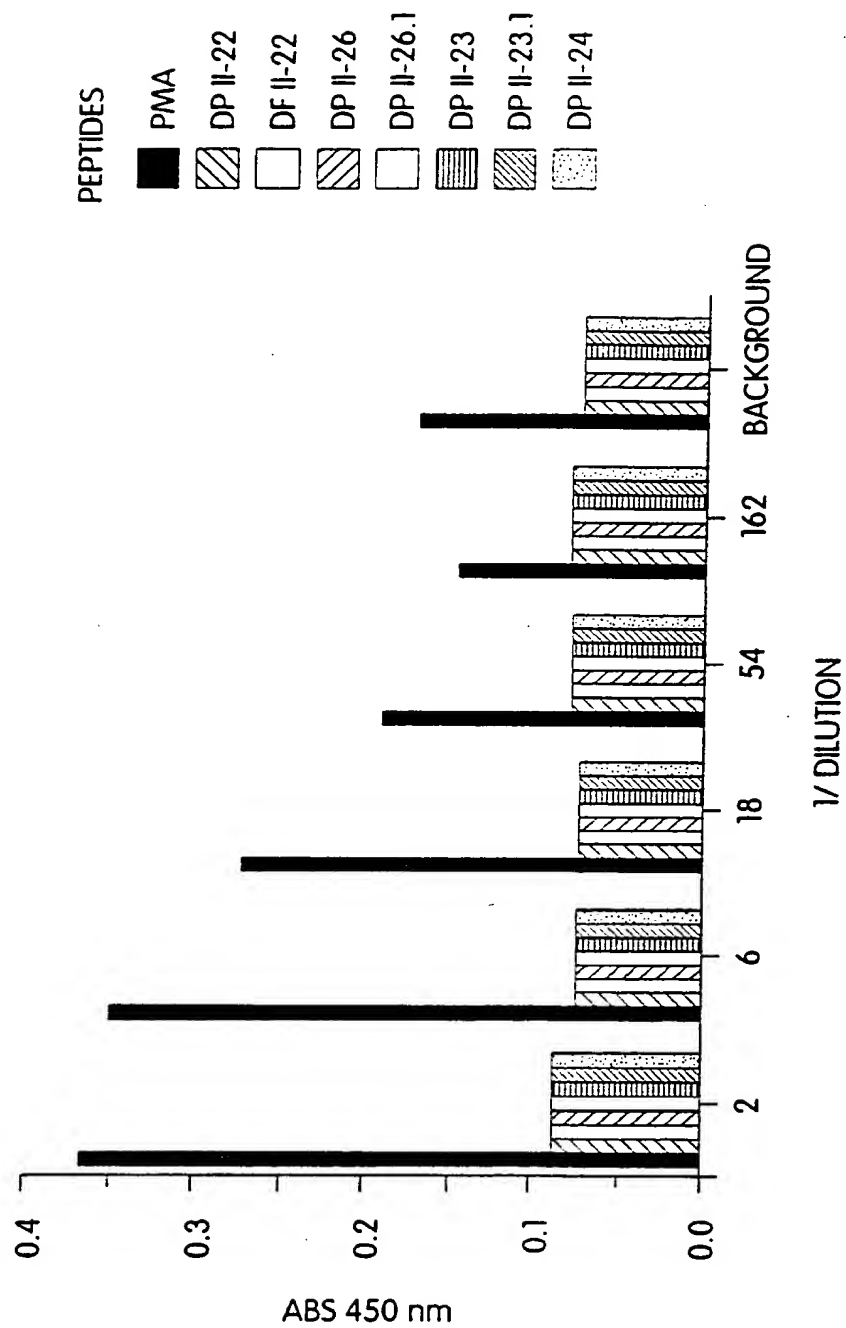


Fig. 21g

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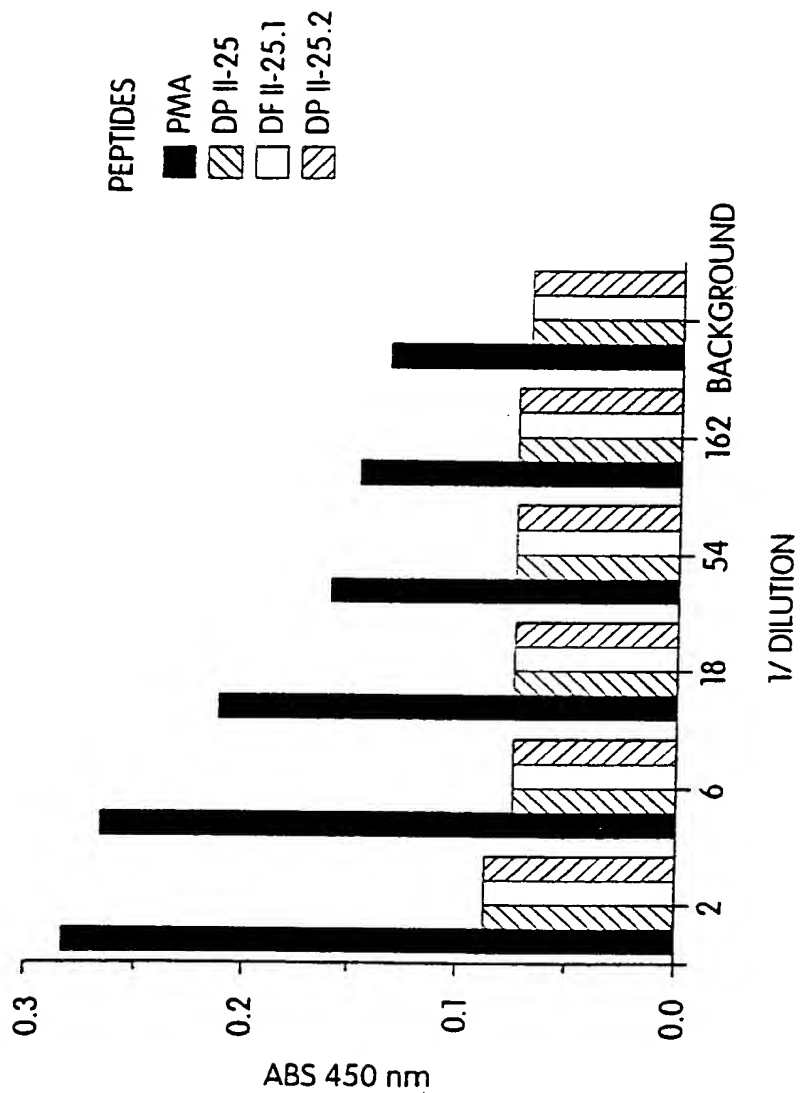


Fig. 21h

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Der p I (a)	10	20	30	40	50	60
Der p I (b)	TNACSINGNA	PAEIDLQRMR	TVTPIRMQGG	CGSCWAFSGV	AATESAYLAH	RNQSLDLAEQ
Der p I (c)	-----	-----	-----	-----	-----Y	-----
Der p I (d)	-----	-----	-----	-----	-----Y	-----
Der p I (e)	-----	-----	-----	-----	-----	-----
Der p I (a)	70	80	90	100	110	120
Der p I (b)	ELVDCASQHG	CHGDTIPRGI	EYIQHNGVVQ	ESYRYVARE	QSCRRPNAQR	FGISNYCQIY
Der p I (c)	-----	-----	-----	-----	-----	-----
Der p I (d)	-----	-----	K-----	-----	-----	-----
Der p I (e)	-----	-----	-----	-----	-----	-----
Der p I (a)	130	140	150	160	170	180
Der p I (b)	PPNANKIREA	LAQTHSAIAV	IIGIKDLDAF	RHYDGRITIQ	RDNGYQPNYH	AVNIVGYSNA
Der p I (c)	---V-----	-----	-----	-----	-----	-----
Der p I (d)	---V-----	-----	-----	-----	-----	-----
Der p I (e)	-----T-----	-----	-----	-----	-----	-----
Der p I (a)	190	200	210	220	IL	
Der p I (b)	QGVYDWIVRN	SWDTNWDNG	YGYFAANIDL	MMIEEYPYVV	IL	
Der p I (c)	-----	-----	-----	-----	---	
Der p I (d)	-----	-----	-----	-----Q-----	---	
Der p I (e)	-----	-----	-----	-----	---	

Fig. 22

Der p II (c)	10	20	30	40	50
(1)	DQVDVKDCANHEIKKVLVPGCHGSEPCIIHRGKPFQLEAVFEANQNTKTAK				
(2)	.....H.....L.P.....E.....Q...V.E...T....				
Der f II	.....H.....L.P.....E.....Q...V.E...S....				
	.....N.....M.D.....D.....T...L.D...T....				
Der p II (c)	60	70	80	90	100
(1)	IEIKASIDGLEVDVPGIDPNACHVMKCPLVKGGQQYDIKYTNVVPKIAPKSE				
(2)	.....I.....P.....YM.....I.....I.....				
Der f II	.....I.....P.....YM.....I.....I.....				
	.....L.....T.....FM.....A.....A.....I				
Der p II (c)	110	120			
(1)	NVVVTVKVMGDDGVLCACAIATHAKIRD				
(2)	.....VM.DD.....A.....I...				
Der f II	.....VM.ND.....A.....L...				
	.....LV.DN.....A.....I...				
	I	G			

Fig. 23



	10	20	30	40	50	60
pFL1	DQVDVKDCANNEIKKVMVPGCHGSEPCIIHRGKPF	FTLEALFDANQNTKAKIEIKASLDGLE				
pFL2	.....N.....	.....I.....				
MT 3	.....N.....	.....I.....				
MT 5	(1-92)	.....S.....	.....I.....	.....I.....	.....I.....	.....I.....
MT18	(1-84)	.....N.....	.....I.....	.....I.....	.....I.....	.....I.....
MT16	(1-70)	.....N.....	.....I.....	.....I.....	.....T.....	.....I.....

Fig. 24

10     |     20     |     30     |     40     |     50     |     60     |  
 3' -- ATTATTGGCATCAAGATTAGACGCATTCGTCATTTATGATGGCCGAACAATCATTTCAA  
  
 I I G I K D L D A F R H Y D G R T I I Q  
  
 70     |     80     |     90     |     100     |     110     |     120     |  
 CCGATAATGGTTACCAAACTGTTAAAGTTCTGGTGATGATGGTGTTTGGCCTCTGCT  
  
 R D N G Y Q T V K V L G D D G V L A S A  
  
 130     |     140     |     150     |     160     |     170     |     180     |  
 ATTGCTACTCATGCTAAAATCCGCGATGTGCGCGAACTGAATCAGCTTATTGGCCTAC  
  
 I A T H A K I R D V A A T E S A Y L A Y  
  
 190     |     200     |     210     |     220     |     230     |     240     |  
 CGTAAACACGTCTTTGGATCTTTCTGTAACAGGAACCTCGTCGATCAATTGGAAGCCGTTTTC  
  
 R N T S L D L S E Q E L V D Q L E A V F  
  
 250     |     260     |     270     |     280     |     290     |     300     |  
 GAAGCCAACCAAAACACAAAACCGCTAAATTTGAAATCAAGCCTCAATCGATGGTTTA  
  
 E A N Q N T K T A K I E I K A S I D G L

Fig. 25

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310 | 320 | 330 | 340 | 350 | 360 |  
 GAAGTTGAATACATCCAAACATAATGGTGTCTCCAAAGAAAGCTACTATCGATACGTTGCA  
 E V E Y I Q H N G V V Q E S Y Y R Y V A  
 370 | 380 | 390 | 400 | 410 | 420 |  
 CGAGAACAAATCATGCCGACGACCAAAATGCACAAAGATCAAGTCGATGTCAAAGATTCTGCC  
 R E Q S C R R P N A Q D Q V D V K D S A  
 430 | 440 | 450 | 460 | 470 | 480 |  
 AATCATGAAATCAAAAAAGTTTGGTACCAGGATCGCATGGTTCAGAAACCAAGTATCAAT  
 N H E I K K V L V P G S H G S E P S I N  
 490 | 500 | 510 | 520 | 530 | 540 |  
 GGAAATGCTCCAGCTGAAATCGATTTCGCGACAAATGCCGAACTGTCACTCCCATTCGTATG  
 G N A P A E I D L R Q M R T V T P I R M  
 CAATAATGA-3'  
 Q - -

Fig. 25 cont.

10 | 20 | 30 | 40 | 50 | 60 |  
5'--ACTGTTAAAGTTCTGGTGATGATGGTGTGTTTGGCCCTCTGCTATGCTACTCATGCTAAA  
T V K V L G D D G V L A S A I A T H A K  
70 | 80 | 90 | 100 | 110 | 120 |  
ATCCGGGATGTTGCCGCAACTGAATCAGCTTATTTGGCCCTACCGTAACACGCTTTTGAT  
I R D V A A T E S A Y L A Y R N T S L D  
130 | 140 | 150 | 160 | 170 | 180 |  
CTTCTGAACAGGAACCTCGTCGATGAATACATCCAACATAATGGTGTCTCCAGAAAGC  
L S E Q E L V D E Y I Q H N G V V Q E S  
190 | 200 | 210 | 220 | 230 | 240 |  
TACTATCGATACGTTGCACGAGAACAAATCATGCCGACGACCAAAATGCACAACAATTGGAA  
Y Y R Y V A R E Q S C R R P N A Q Q L E  
250 | 260 | 270 | 280 | 290 | 300 |  
GCCGTTTTCGAAGCCAAACCAAAACACAAAACGGCTAAAATTGAAATCAAAGCCTCAATC  
A V F E A N Q N T K T A K I E I K A S I

Fig. 26

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310 | 320 | 330 | 340 | 350 | 360 |
GATGGTTAGAAAGTTATATTGGCATCAAGATTAGACGCATTCCGTCATTATGATGGC

D G L E V I I G I K D L D A F R H Y D G

370 | 380 | 390 | 400 | 410 | 420 |
CGAACAATCATCAACGCGATAATGGTTACCAAGTATCAATGGAAATGCTCCAGCTGAA

R T I I Q R D N G Y Q S I N G N A P A E

430 | 440 | 450 | 460 | 470 | 480 |
ATCGATTGCGACAAATGCGAACTGTCACTCCCATTCGTATGCAAGATCAAGTCGATGTC

I D L R Q M R T V T P I R M Q D Q V D V

490 | 500 | 510 | 520 | 530 | 540 |
AAAGATTCTGCCAATCATGAAATCAAAAAGTTTGGTACCAGGATCGCATGGTTCAGAA

K D S A N H E I K K V L V P G S H G S E

CCATAATGA-5'

P - -

```

Fig. 26 cont.

10 | 20 | 30 | 40 | 50 | 60 |  
 5'-ACTGTTAAAGTTTGGGTGATGATGGTGTGTTTGGCCCTCAGCTATTGCTACTCATGCTAAA  
  
 T V K V L G D D G V L A S A I A T H A K  
  
 70 | 80 | 90 | 100 | 110 | 120 |  
 ATCCGCGATAGTATCAATGGAAATGCTCCAGCTGAAATCGATTGCGACAAATGCCGAACT  
  
 I R D S I N G N A P A E I D L R Q M R T  
  
 130 | 140 | 150 | 160 | 170 | 180 |  
 GTCACCTCCCATTCGTATGCAAGAATACATCCAACATAATGGTGTCTCGTCCAAAGAAAGCTAC  
  
 V T P I R M Q E Y I Q H N G V V Q E S Y  
  
 190 | 200 | 210 | 220 | 230 | 240 |  
 TATCGATACGTTGCACGAGAACAAATCATGCCGACGACCAAAATGCACAAATTATTGGCATC  
  
 Y R Y V A R E Q S C R R P N A Q I I G I  
  
 250 | 260 | 270 | 280 | 290 | 300 |  
 AAAGATTAGACGCAATCCGTCATTATGATGGCCGGAACAATCATTCACGCGATAATGGT  
  
 K D L D A F R H Y D G R T I I Q R D N G

Fig. 27

310 | 320 | 330 | 340 | 350 | 360 |  
TACCAACAATTGGAAGCCGTTTTCGAAGCCAACCAAAACAAAAACGGCTAAATTTGAA  
Y Q Q L E A V F E A N Q N T K T A K I E  
370 | 380 | 390 | 400 | 410 | 420 |  
ATCAAAGCCTCAATCGATGGTTTAGAAGTTGATCAAGTCGATGTCAAAGATTCAGCCAAT  
I K A S I D G L E V D Q V D V K D S A N  
430 | 440 | 450 | 460 | 470 | 480 |  
CATGAAATCAAAAAAGTTTGGTACCAGGATCACATGGTTCAGAACCCAGTTGCCGCAACT  
H E I K K V L V P G S H G S E P V A A T  
490 | 500 | 510 | 520 | 530 | 540 |  
GAATCAGCTTATTGGCCCTACCGTAACACAGTCCTTTGGATCTTCTGAAACAGGAACCTCGTC  
E S A Y L A Y R N T S L D L S E Q E L V

GATTAGTAG-5'

D - -

Fig. 27 cont.

DP	I-23.1	EYIQHNGVVQESYRYVAREQSCRRPNAQ
DP	I-23.1.1	KKEYIQHNGVVQESYRYVAREQSCRRPNAQ
DP	I-23.1.2	KEYIQHNGVVQESYRYVAREQSCRRPNAQ
DP	I-23.1.3	EYIQHNGVVQESYRYVAREQSSRRPNAQ
DP	I-23.1.4	EYIQHNGVVQESYRYVAREQSERRPNAQ

DP	II-22	QLEAVFEANQNTKTAKIEIKASIDGLEV
DP	II-22.1	KKQLEAVFEANQNTKTAKIEIKASIDGLEV
DP	II-22.2	KQLEAVFEANQNTKTAKIEIKASIDGLEVK

Fig. 28



## INTERNATIONAL SEARCH REPORT

International Application No

PCT/US 92/08637

<b>I. CLASSIFICATION OF SUBJECT MATTER</b> (If several classification symbols apply, indicate all) <sup>6</sup>		
According to International Patent Classification (IPC) or to both National Classification and IPC		
Int.Cl. 5 C12N15/12; C07K7/10;	A61K39/35; C07K15/08	C12N15/62; G01N33/53
<b>II. FIELDS SEARCHED</b>		
Minimum Documentation Searched <sup>7</sup>		
Classification System	Classification Symbols	
Int.Cl. 5	C07K ; C12N ; A61K	
Documentation Searched other than Minimum Documentation to the Extent that such Documents are Included in the Fields Searched <sup>8</sup>		
<b>III. DOCUMENTS CONSIDERED TO BE RELEVANT<sup>9</sup></b>		
Category <sup>10</sup>	Citation of Document, <sup>11</sup> with indication, where appropriate, of the relevant passages <sup>12</sup>	Relevant to Claim No. <sup>13</sup>
X	<p>ANNUAL REVIEW OF IMMUNOLOGY vol. 9, 1991, PALO ALTO, CA US pages 67 - 95 O'HEHIR, R.E. ET AL. 'The specificity and regulation of T-cell responsiveness to allergens' cited in the application see the whole article, especially page 71: 'Mapping of T-cell epitopes', epitope His(85)-Asp(109)</p> <p style="text-align: center;">---</p> <p style="text-align: right;">-/--</p>	10, 14, 16-18
<p><sup>10</sup> Special categories of cited documents:</p> <p>"A" document defining the general state of the art which is not considered to be of particular relevance</p> <p>"E" earlier document but published on or after the international filing date</p> <p>"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)</p> <p>"O" document referring to an oral disclosure, use, exhibition or other means</p> <p>"P" document published prior to the international filing date but later than the priority date claimed</p> <p>"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention</p> <p>"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step</p> <p>"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.</p> <p>"&amp;" document member of the same patent family</p>		
<b>IV. CERTIFICATION</b>		
Date of the Actual Completion of the International Search		Date of Mailing of this International Search Report
18 JANUARY 1993 ,		
International Searching Authority		Signature of Authorized Officer
EUROPEAN PATENT OFFICE		ANDRES S.M.

III. DOCUMENTS CONSIDERED TO BE RELEVANT (CONTINUED FROM THE SECOND SHEET)		
Category °	Citation of Document, with indication, where appropriate, of the relevant passages	Relevant to Claim No.
X	WO,A,8 810 297 (PRINCESS MARGARET CHILDREN'S MEDICAL RESEARCH FOUNDATION (INC.) ET AL.) 29 December 1988	16-18, 32-33, 65-66, 93-95
Y		22
A	see page 2, line 15 - line 28	1-20, 38-55, 61-66
	see page 14 - page 15; example 4	71-83, 93-95
Y	FR,A,2 437 837 (THE JOHNS HOPKINS UNIVERSITY) 30 April 1980 see the whole document	22
X	EP,A,0 410 848 (LABORATOIRE DES STALLERGENES) 30 January 1991 see the whole document	84, 93-95
A		62-77, 84-95
A	EP,A,0 445 971 (ASAHI BREWERIES, LTD.) 11 September 1991 see the whole document	1, 26-28, 35-55 61-64, 66-68, 71-79, 82-85, 89-90, 93-95
A	CLINICAL AND EXPERIMENTAL ALLERGY vol. 21, January 1991, pages 25 - 32 DILWORTH, R.J. ET AL. 'Sequence analysis of cDNA coding for a major house dust mite allergen, Der f I' cited in the application see the whole document	1, 26-29, 32-33, 35-41, 44-55, 61-63, 67-68 71-79, 84-86, 89-91, 93-95
P,X	WO,A,9 204 445 (THE WESTERN AUSTRALIAN RESEARCH INSTITUTE FOR CHILD HEALTH LTD.) 19 March 1992 see page 8, line 29 - page 9, line 30 see page 19 - page 24, line 8	1, 4-9, 62-64 84, 89 93-95

-/--

III. DOCUMENTS CONSIDERED TO BE RELEVANT (CONTINUED FROM THE SECOND SHEET)		
Category *	Citation of Document, with indication, where appropriate, of the relevant passages	Relevant to Claim No.
P,X	JOURNAL OF IMMUNOLOGY vol. 148, no. 3, 1 February 1992, BALTIMORE US pages 738 - 745 YSSEL, H. ET AL. 'T cell activation-inducing epitopes of the house dust mite allergen Der p I' cited in the application see the whole article, and especially from page 743, last paragraph to the end ---	1,4-9
A	WO,A,9 106 571 (IMMULOGIC PHARMACEUTICAL CORPORATION) 16 May 1991 see the whole document -----	

**Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)**

This international search report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☒ Claims Nos.:  
because they relate to subject matter not required to be searched by this Authority, namely:  
Remark: Although claims 63-64, 66, 68, 70, 72-73, 75, 77, 89-92, 95 are directed to a method of treatment of (diagnostic method practised on) the human/animal body the search has been carried out and based on the alleged effects of the compound/composition.
2. ☐ Claims Nos.:  
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:
3. ☐ Claims Nos.:  
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

**Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)**

This International Searching Authority found multiple inventions in this international application, as follows:

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☐ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
- ☐ No protest accompanied the payment of additional search fees.

**ANNEX TO THE INTERNATIONAL SEARCH REPORT  
ON INTERNATIONAL PATENT APPLICATION NO.**

US 9208637  
SA 65713

This annex lists the patent family members relating to the patent documents cited in the above-mentioned international search report. The members are as contained in the European Patent Office EDP file on  
The European Patent Office is in no way liable for these particulars which are merely given for the purpose of information.

18/01/93

Patent document cited in search report	Publication date	Patent family member(s)		Publication date
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		EP-A-	0500785	02-09-92
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